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GenCore version 5.1.6
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Copyright (c) 1993 - 2003 Compugen Ltd.	OM nucleic - nucleic search, using sw model	November 25, 2003, 22:28:25; Search time 5208.63 Seconds (without alignments) 16556.656 Million cell updates/sec	US-09-852-209A-2 : 2108 1 cccgccgtgagtgagctctncttttttgaaataataa 2108	: IDENTITY NUC Gapop 10.0 , Gapext 1.0	2888711 seqs, 20454813386 residues
	OM nucleic - r	Run on:	Title: Perfect score: Sequence:	Scoring table:	Searched:

Total number of hits satisfying chosen parameters: 5777422
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : GenEmbl:\*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	escription	44813	10624	AR232022 Sequence	47650	91260	AX464152 Sequence	AX234498 Sequence	AF091434 Homo sapi	Segue	AF260738 Homo sapi	Seque	ŧΛ	ďΛ	seque	Тошо	BD004757 Novel VEG	Antib	AC092608 Homo sapi	AX027935 Sequence	segue	Mus		Segu	rΛ	ďΩ	CO		_	AF286725 Mus muscu	AB033829 Gallus ga	AR282950 Sequence	S)		AX027960 Sequence	EST a		Segue	AX027962 Seguence				0.62	1993 Sequenc	ω	6861	•
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### ALIGNMENTS

	PRI 27-AUG-2001	complete cds.					
	AF244813 2152 bp mRNA linear	Homo sapiens platelet-derived growth factor C mRNA, complete cds.	AF244813	AF244813.1 GI:8886883		Homo sapiens (human)	ORGANISM Homo sapriens
RESULT 1 AF244813	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM

Homo saptens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Catarrhini, Hominidae, Homo.
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
I (basea I to 2.152)
Li.X., Ponten, A., Aase, K., Karlsson, L., Abramsson, A., Uutela, M.,
Backstrom, G., Hellstrom, M., Bostrom, H., Li, H., Soriano, P.,
Betsholtz, C., Heldin, C.-H., Alitalo, K., Ostman, A. and Eriksson, U.

REFERENCE AUTHORS

840

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us-09-852-209a-2.rge

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CTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGGATAGCCGCAT 1080
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                          633 TATTTCCTTCTGAACCAGGTTCTGCATCCACTACAACATGTCATGCCACAATTTCACA 692
                                                                                  541 GAAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATAAT 600
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  481 YATTTTCCTTCTGAACCAGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCACA 540
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ICKYDFVEVEERPSDGTILGRMCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGRCIHY
NIVMPQFTEAVSPSVLPPSALPLDLINNAITARSTLEDLIRYLEPERWQLDLEDLYRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation≈"MSLFGLLLVTSALAGQRRGTQAESNLSSKFQFSSNKEQNGVQDP
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VKRCGGUCACCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEE
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factor receptor alpha (PDGRRalpha)"
factor, imember of the PDGF/VEGF growth factor
family; contains N-terminal CUB domain and the C-terminal
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                                                                                                        2 (bases 1 to 2152)
Briksson, U., Aase, K., Li, X. and Ponten, A.
Direct Submission
Submitted (14-WAR-2000) Ludwig Institute for Cancer Research,
Nobels vag 3 P.O. Box 240, Stockholm S-171 77, Sweden
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.9%; Score 1999.6; DB 9; Length 2152; 100.0%; Pred. No. 0; 1.00.0%; Pred. No. 0; Mismatches 0; Indels 0;
PDGF-C is a new protease-activated ligand for the PDGF
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/product="platelet-derived growth factor C"
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                                        Nat. Cell Biol. 2 (5), 302-309 (2000)
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nol_type="mxbx"
db_xref="taxon:9606"
/tissue_type="lung"
dev_stage="fetal"
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/db_xref="GI:8886884"
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function="ligand
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                       alpha-receptor
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/organism="unknown" BASE COUNT 849 a 522 c 605 g 848 t 1 others ORIGIN	Query Match 93.9%; Score 1979.4; DB 6; Length 2825; Best Local Similarity 97.7%; Pred. No. 0; Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;	2.2 CCGCCGTGAGTGAGCTCTCACCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCT	62 TGACATCTGCCCTGGCCGGCCAGAGGGGGGGGACTCAGGGGGAATCCAACCTGAGTAGTA 1	122	1887	242 GAATACGTCTTGGTATGGAGTTTGTCCCCGGAAATTTGTGTATGGAGTTACAGGAAAATTTATGAACTTACAGAAAAATTTATGAAGAAAAATTAAGTAGAGAAAAATTAAGAAAAATTAAAAAA	302 COTTIGATORANGATITICGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATTTTG 36	362 TAGAAGTTGAGAACCCAGTGAACTATATTAGGGCCTGGTGTGTTCTGTTTTG CO	422 TACCAGGAAACAGATTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCGAATGAAT	482 ATTTCCTTCGAACCAGGGTTCTGCATCCACTACAACATGTCATCACAG 704 ATTTTCCTTCTGAACCAGGGTTCTGCATCCACTACAACATTGTCATGCAACATTGTCACAG 704 ATTTTCTTCTTCAACATTGTAACATTGTAACAATTGTCATGAACAATTGTCAACAATTGTCAACAATTGTAACAATTGTAACAACAATGTCAACAAT	542 AAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATG		662 AGTIGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTGGCAAGAGTTTTGTTT   High	QY 722 TIGGAAGAAAATCCAGAGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACA 781	Qy 782 GCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCA 841	OY 842 ITITCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGGAACTGTGCCTGTTGTCTCC 901	2y 902 ACAATTGCAATGAATGTCAATGTCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCC 961	Db 1124 ACANTIGCAATGAATGTCAATGTGCCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCC 1183	Qy 962 TTCAGTTGAGACCAAAGACCGGTGTCAGGGGATTGCACAAATCACTCAC
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Hillan,K.J., Kuo,S.S., Tumas,D. and Wood,W.I.
Compositions and methods for the treatment of immune related
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity 97.7%; Pred. No. 0;
Matches 2059; Conservative 1; Mismatches 36; Indels 11;
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/organism="Homo sapiens"
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Promotion or inhibition of angiogenesis and cardiovascularization Patent: Wo 007345-A 3 07-DEC-2000;
Genentech Inc. (US)
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Mammalia, Butheria, Primates, Catarthini, Hominidae, Homo.
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/organism="Homo sapiens"
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1750 AAAATGTATAAAATCTGGATTTTTTTTTTTTTTTTGCTCATATTCACATATGTAAACC 1809
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                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.9%; Score 1979.4; DB 6; Length 2849; 97.7%; Pred. No. 0; ive 1; Mismatches 36; Indels 11;
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Genentech Inc. (US)
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db xref="taxon:9606"
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                                                          Homo sapiens (human)
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Best Local Similarity 97.7
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                                                                                                                                     TIATTACTGTGTGTACTAATGGAAGTATTCACAGGCCCAAGGTTTCCTCATACTTATCCAA 241
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                                              AATTCCAGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAA 181
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ICKYDPVBVEBESDGTILGRWCGSGTVPGKQISKGNQIRIRRYSDBYPPSBEGFCIHY
NIVMDQFTBAVGPSYLDPSALPIDLIMNAITARSTLEDLIRYLBPERWQLDLEDLYRP
TWOLLGKAFVFGRKSRYVDLALLTERYRLYSCTPRNFSYSIRELKKTDTIFWGCLL
VKRCGGNCACCLIHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/protein_id="CAC69781.1"
/db_xref="GI:1593482"
/trenslation="MSLFGLLLLTSALAGQRQCTQAESNLSSKFQFSSNKEQNGVQDP
                          1802 CTCCTTTGACATTATAACTGTTGCCTTTTCTAATCTTGTTAATATATCTTTTTTACC 1861
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                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTTAAAAAACTGAATT----GGAATAGAATTGGTAAGTT----GCAAAGACTTTTTGAAAA 2338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAT 11-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Materiais and methods involving hybrid vascular endothelial growth factor dinas and proteins and soreening methods for modulators Patent: WO 0162942-A 143 30-AUG-2001; LUDWIG INSTITUTE FOR CANCER RESEARCH (US) ; Licentia OY (FI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     457 CCCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCAAATGAGCCTCTTCGGGGCTTCTCCTGC 516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                    1862 AAAGGTATTTAATATTCTTTTTTATGACAACTTAGATCAACTATTTTTAGCTTGGTAAAT
                                                                                                                                               2110 AAAGGTATTTAATATTCTTTTTTATGACAACTTAGATCAACTATTTTAGCTTGGTAAAT
                                                                                                                                                                                                                                        1982 CTGGACAAAATACATGTATNTCCATCCCGGAATGGTGCTAGAGTTGGATTAAACCTGCA
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1; Mismatches 36; Indels 11; Gaps
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/note="unnamed protein product"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 148 from Patent W00162942. AX234498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic_DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alitalo, K.M. and Jeltsch, M.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1562 AGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAATTAA 1621
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                                                                                              TIGIATIAAAIAGAICACCAGCIAGIIITCAGAGIITACCAIGIACGIATICCACIAGCIGG 1381
                                                                                                                                                                                                                                                                                                                                                                                                     1777 TTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGG 1836
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AFU91434 3007 bp mRNA linear PRI 22-JUN-2000 Homo sapiens secretory growth factor-like protein fallotein mRNA, complete cds.

AF091434.1 GI:6002592

VERSION

AF091434

DEFINITION ACCESSION

RESULT 8 AF091434

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                                     Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 3007)
1 Tasi, Y.J., Lee, R.K., Lin, S.P. and Chen, Y.H.
1 Identification of a novel platelet-derived growth factor-like gene, fallocein, in the human reproductive tract
Biochim. Biophys. Acta 1492 (1), 196-202 (2000)
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Tsai,Y.J., Lee,R.K.K. and Lin,S.P.
Direct Submission
Submitted (14-SEP-1998) Dept. Medical Research, Mackay Memorial
Hospital, 45 Min Sheng Road, Tamshui, Taipei County 25115, Taiwan
Location/Qualifiers
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/note≈"found in female reproductive tract"
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Best Local Similarity 97.7%;
Matches 2059; Conservative 1
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	RESULT 9  AX73931 LOCUS LOCUS LOCUS LOCUS DEFINITION Sequence 3 from Patent W003024478.  DEFINITION Sequence 3 from Patent W003024478.  DEFINITION Sequence 3 from Patent W003024478.  ACCESSION AX73931. GI:30519211  VERNIONS SOURCE Homo sapiens (human) ORGANISM Homo sapiens (human)  REFERENCE AMMMANILA; Putheria; Primates; Catarrhini; Hominidae; Homo.  REFERENCE AUTHORS Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.  TITLE AUTHORS Neather: Wo 03024478-A. 3.27-MAR-2003;  TITLE Treatment of central nervous system disorders by use of pdgf or Coation/Qualifiers  JOURNAL Patent: W0 03024478-A. 3.27-MAR-2003;  FATURES  L. 180   Location/Qualifiers  L. 180   Location/Qualifiers  Mol type="genomic DNA"   ABASE COUNT   Ab Ared: "Accession of the complete of the complete of the coation of
422 TACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGATGATT 482 TATCTCCTCTGAACAGATTTCTAAAGGAAATTAGGATAAGATTTGTATCTGATGAAAA 482 ATTTTCCTTCTGAACAGATTTCTCATCCACTACAAATTAGGATTAGTACTGAAAATCAGAGATTTCTCAACAGATTCTCAACAGATTTCAACAGATTCTCAGAGATTTCAACAGATTCTCAGAGATTCTAGAGATTTTTCTCATCTTTAGACCTTTAATTAA	

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CCCGCCGTCAGTCAGCTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTGG 61		TAGAAGTTGAGGAACCCAGTGATGGAACTATATAGGGCGCTGGTGTGGTGTTGGTACTG	AAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGGTTAATAATG  [	
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HOMO Sapiens platelet-derived growth factor C (PDGFC) mRNA, complete cds.
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                                                                                                 1268 ATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGAT 1327
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1 (bases 1 to 1804)
2 (diberteon, D.G., Duff, M.E., West, J.W., Kelly, J.D., Sheppard, P.O., Hofstrand, P.D., Gao, Z., Shoemaker, K., Bukowski, T.R., Moore, M., Feldhaus, A.L., Humes, J.M., Palmer, T.B. and Hart, C.E. Platelet-derived growth factor C (PDGF-C), a novel growth factor J. Binds to PDGF alpha and beta receptor J. Binds to PDGF alpha and beta receptor J. Biol. Chem. 276 (29), 27406-27414 (2001)
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Gao,Z., Hart,C., Piddington,C., Sheppard,P., Shoemaker,K.,
Gilbertson,D., West,J. and O'Hara,P.J.

Direct Submission
Submitted (126-APR-2000) Biomolecular Informatics, ZymoGenetics,
Inc., 1201 Eastlake Avenue East, Seattle, WA 98102, USA
Location/Qualifiers
                                                                               1142 AIGCGTTATCTCCATCCTTAATCTCAGTTTTGCTTCAAGGACCTTTCATCTTCAGGAT
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AF260738.1 GI:14009503
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AUTHORS
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KEYWORDS
SOURCE
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patent US 6495668.
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/product="platelet-derived growth factor C"
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ICKYDFWSPERSPSVLPPSALPLDLINNAITAFSTLEDLIRYLEPERWQLDLEDLYRP
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                                   /gene="PDGFC"
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Gilbert,T., Hart,C.E., Sheppard,P.O. and Growth factor homolog ZVEGF4
Patent: US 649568-A 32 17-DEC-2002;
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Patent: WO 0066736-A 32 09-NOV-2000;
ZymoGenetics, Inc. (US)
Location/Qualifiers linear /note="unnamed protein product" /codon\_start=1 /protein\_id="CAC17170.1" DNA AX044518 1760 bp Sequence 32 from Patent WO0066736. AX044518 AX044518.1 GI:11343373 /organism="Homo sapiens" /mol\_type="genomic DNA" /db\_xref="taxon:9606" 1547.1191

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                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
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Patent: WO 0128586-A 1 26-AFR-2001;
ZymoGenetics, Inc. (US)
Location/Qualifiers
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Spinal cord-derived growth factor; scdgf gene.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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ATTITCCTICTGAACCAGGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCACAG
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Submitted (25-OCT-1999) Tsuyoshi Hamada, Nippon Medical School,

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Tel:81-3-3822-2131(ex.5277), Fax:81-3-5814-1684)

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0; Mismatches 13;
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A novel gene derived from developing s
unique member of the PDGF/VEGF family
FBBS Lett. 475 (2), 97-102 (2000)
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Hamada,T., Ui-Tei,K. and Miyata,Y.
Direct Submission
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	cDNA encoding plat	Human VEGF-E DNA.	DNA encoding human	Human TANGO 128 co	Human PRO200 nucle	Human PRO200 (UNQ1	Human PRO200 (VEGF	Human PRO200 prote
Ω	AA12523	AAZ23691	ABS57294	AAA47452	AAZ34296	. AAC78582	. AAA88515	. AAC58579
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Human PRO713 cDNA	Human cDNA se	PR0200	Human PRO200 codi					cDNA encodin			cDNA encodi	Bone m	Human vascula	Human VEGF-X	Human VEGF-X	Human		DNA encoding		Bone morphoge	Human	Human	9 Human	2 Human cDNA en		6 DNA encoding hum	4 CDNA e	Human	Human VEGF/P	Human VEGF-X	Human VEGF-X	Human VEGF-X	Human VEGF-X		
AAA77623	AAS21386		AAC88962	AAC97404	ACA0374	ACA04166	ABX89283	ABX92668	AAS12884	AAA71951	AAA52458	AAZ48599	ABQ81461	AAA71990	AAA71952	AAD06812	AAC64426	AAX86352	AAF18314	AAZ48600	AAC81582	AAA51498	AAD0464	ABS6861	AAI7244	ABX9314	AAA1252	AAF82259	ABN8897	AAA71955	AAA71936	AAA71982	AAA71983	AAA71989	
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#### ALIGNMENTS

AAA12523 standard; cDNA; 2108 BP.

RESULT 1

**AAA1252**3

AAA12523;

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Platelet-derived growth factor C; PDGF-C; cell proliferation, growth factor; heparin; connective tissue; wound healing; VEGF-F; fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth; choriccarcinoma; Wilms tumour; megakaryoblastic leukaemia; lung carcinoma; erythroleukemia; tissue remodelling; ss.
                                                                                                                                                                        Location/Qualifiers
37.1073
74.tag = a
/product= "platelet-derived growth factor C"
                                                     CDNA encoding platelet-derived growth factor C (PDGF-C).
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CD proliferation, preferably in combination with one other growth factor and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also be used for stimulating commediate processed to generate the active truncated form of PDGF-C and used to receptor-binding cpells comprising to an also be used to promote fibror of promoted form of PDGF-C and used to rinding the receptor-binding specificity of PDGF-C and be used to inhibit tumour growth of a tumour corporation. CC antagonists can be used to inhibit tumour growth of a tumour cexpressing PDGF-C in a mammal. Specific types of human tumours, e.g. choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma and erythroleukemia, can be identified by testing for expression of control production of remour cells into a normal population of remodelling during invasion of treat fibrotic conditions,
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Betsholz C;
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UNIV HELSINKI LICENSING LTD
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This invention describes the isolation of a novel human vascular endothelial cell growth factor-E (VEGF-E) polypeptide which has candothelial cell growth factor-E (VEGF-E) polypeptide which has tranquilizer, vulnery and cardiant activity. VEGF-E can be administered therapeutically, especially by expressing encoding polynucleotides, to treat cardiovascular or endothelial disorders in mammals, especially humans. It is useful in wound repair and tissue generation and cardiovascular or endothelial disorders in mammals, especially to treat disorders as above. VEGF-E can be used to screen for antagonists and agonists, and the antagonists administered to treat angiogenic disorders in mammals (especially humans) e.g. cancer or seren for antagonists and agonists, and the antagonists and agonists, concerting the antibodies.

CC treat angiogenic disorders in mammals (especially to diagnose cardiovascular, endothelial or angiogenic disorders in mammals (e.g. useful to detect VEGF-E polypeptide, especially to diagnose cardiovascular disease, or neovascularization associated with tumor formation by contacting the antibody with a tissue sample and detecting the antibody with a tissue sample and detecting the antibody with a tissue sample and endothelial disorders in mammals, by detecting abnormally high or low VEGF-E gene expression in the samples. They can also be used to diagnose a disease or this succeptibility to a disease related to a mutated form of vector and samples. They may also be used to produce probes useful to detect related as a sample. They may also be used to produce probes useful to detect related as a sample. They may also be used to produce probes useful to detect related to a sample. They may also be used to produce probes useful to detect related to a sample of the probes useful to detect well as a sample of the probes useful to detect well as a sample of the probes useful to detect well as a sample of the probes useful to detect well as a sample of the probes useful to detect well as a second to the pro
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Best Local Similarity 97.7%;
Matches 2059; Conservative
                                             98US-0040220.
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                                                                                                                       (GETH ) GENENTECH INC.
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                                                       1501 TAAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTGCTCATATTCACATATGTAAAC
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                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding endothelial cell growth factor-E polypeptide, useful for diagnosing or treating a cardiovascular, endothelial or angiogenic disorder such as cancer, diabetes mellitus or atherosclerosis -
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Pred. No. 0;
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                                                                                                                                                                                               Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host diseases, rheumatoid arthritis, postriasis, inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous leukemia, cancer, liver disease, Hodgkin's chronic myelogenous leukemia, cancer, liver disease, Hodgkin's chronic myelogenous leukemia, cancer, liver disease, Hodgkin's disease e.g. myasthemia gravis, autoimmune diabetes and systemenic lupus erythematosus. The nucleic acids are also useful for producing transgenic animals and the TANGO polypeptides themselves. Partial TANGO-18, 140, 197, 212, 213, 224, 239 sequences are useful in forensic biology, for diagnostic assays, prognostic assays, pharmacogenomics and for monitoring clinical trials. TANGO polypeptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a disorder associated with aberrant TANGO expression. A wide range of cellular disorders can be treated.
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1; Mismatches
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3-2   AAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATG 601   7-9-3   AAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATG 652   602   CTATAACTGCCTTTAGTACCTTGGAAGACTTGTCACCTGGACCTGGCTTAATAGTG 652   613   CTATAACTGCCTTTAGTACCTTGGAAGACTTCTTGGAACCTGGCTTAATAGTG 611   614   615   616   616   617	1082   ACCACCAGCACCTCTGCCCACAGCTGCAGTGCAGTGCTGATTCTATTACAGAACGT   1313   ACCACCAGCAGCTCTTGCCCAGAGCTGCTGCTGTGCTTCTATTCTATTGAGAACGT   1392   ACCACCAGCAGCTCTTGACTTCTATTCTCTTTAGAGAACGT   1201   1393   ACCACCAGCAGCTCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGAT   1201   1423   ATCAGTTATCTCCATCATCTAAACAGAACACACACACTCTTCAGGAT   1201   1423   ATCAGTTCTCTCCATCATCTAAACAGAACACACACACTCTTCAGATTTAAACACACAC

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309 369 489 699 849 62 TGACATCTGCCCTGGCCGGCCAGAGGACGAGCTCAGGCGGAATCCAACCTGAGTAGTA 121 181 429 241 301 549 361 609 421 481 729 541 789 601 61 CCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTGC 310 TGACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTAGTA TIATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCAA GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACTTA CCCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTGG CGTTTGATGAAAGATTTGGGCCTTGAAGACCCAGAAGATGACATATGCAAGTATGATTTTG CGTTTGATGAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATTTTG TAGAAGTIGAGGAACCCAGIGAAGTATATATAAGGCGCTGGTGTGGTTCTGGTACTG AAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATG TAGAAGTTGAGGAACCCAGTGATGGAACTATATAAGGGCGCTGGTGTGTTCTGGTACTG TACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAAT ATTITICCITICIGAACCAGGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCACAG AAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATG 11; Gaps DB 20; Length 2849; 36; Indels Score 1979.4; Pred. No. 0; 1; Mismatches Query Match Best Local Similarity 97.7%; Matches 2059; Conservative ~ 250 122 370 182 430 490 550 730 542 790 242 302 362 610 422 670 482 ò 셤 ⋩ a à 셤 à g ò d à q 8 g à g ð 셤 g ð

CTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGATGGC 661

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AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bisoactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting the polypeptide for specific targeting. The polypeptide targeting the polypeptide pairs provide specific targeting of bisoactive molecules to cells. AAC78600 to AAC78877 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences.
                                                                                                                                                                                                                         Novel PRO polypeptides and polynucleotides used in detection methods, to target bioactive molecules to specific cells, and to modulate cellular activities -
Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ; Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                           Claim 2; Fig 206; 636pp; English.
                                                                                                                                                      WPI; 2000-611443/58.
P-PSDB; AAB44322.
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# Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;

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셤	820	CTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGATGGC 909
δ	662	AGTIGGACTIAGAAGAICIATATAGGCCAACITGGCAACTICTIGGCAAGGCTITIGITT 721
QQ	910	<u>AGTIGGACITAGAAGAICTATATAGGCCAACTIGGCAACTICTIGGCAAGGCTTTTGTTT 969</u>
ò i	722	
ag	970	TIGGAAGAAATCCAGAGIGGIGGAICIGAACCTICIAACAGAGGAGGAGGAATAATAA 1029
ò	782	
qq	1030	GCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCA 1089
Š	842	TITITCIGGCCAGGITGICTCCTGGITAAACGCTGITGGGAAACTGIGCCTGITGICTCC 901
Ωp	1090	THITCTGGCCAGGITGTCTCCTGGTTAAACGCTGTGGGAACTGTGCCTGTTGTCTCC
λ	905	
Ωp	1150	ACAATTGCAATGAATGTCAATGTCCCAAGCAAAGTTACTAAAAATACCACGAGGTCC 1209
Š	962	
qq	1210	TTCAGTTGAGACCAAAGACCGGTGTCAGGGGATTGCACAAATCACTCAC
ò	1022	TGGAGCACCATGAGGAGTGTGACTGTGTGCAGAGGAGGCACAGGAGAAAAGCCGCATC 1081
ΩÞ	1270	TGGAGCACCATGAGGAGTGTGTGTGTGTGTGGGGGGGGCACAGGAGGATAGCCGCATC 1329
δ	1082	ACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCAGTG
qa	1330	ACCACCAGCAGCTCTTGCCCCAGAGCTGTGCTGTGTGTGT
ζζ	1142	AUGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGAT 1201
qq	1390	
ò	1202	TTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTT 1261
qq	1450	TTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTT 1509
λ	1262	TTGRGAGGGGGCCTAAAGGACGGGGAAAAGGTCTTCAATCGTGGAAAGAAA
Db	1510	TTGAGAGGCCTAAAGGACAGGAGAAAGGTCTTCCATCGTGGAAAGAAA
δ	1322	TTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGGTGG 1381
Db	1570	ifgiatriaaatasaicaccasciastricasasitaccaistacsaartecactasciss
δ	1382	
qq	1630	
ò	1442	
Ωp	1690	TGCAAGTGAGCACCTGATTCCGTTGCCTTAACTCTAAAGCTCCATGTCCTGGGCCT 1749
δ	1502	AAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTGCTCATATTCACATATGTAAACC 1561
ΩÞ	1750	AAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTGCTCATATTCACATATGTAAACC 1809
δ	1562	AGAACATICTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAATTAA 1621
qa	1810	AGAACATICTAIGTACTACAAACCTGGTITTIAAAAAGGAACTATGTIGCTATGAATAA 1869
ò	1622	ACITOBECREGEGATAGGACAGACTGGATTTTCATATTTCTTATAAATTTCTGCC 1681
QC CD	1870	ACTIGIGICALGCIGALAGGACAGACIGGALTITICALATITCTIATIAAATITICIGCC 1929
δλ	1682	ATTTAGAAGAAGAACTACATTCATGGTTTGGAAGAGATAAACCTGAAAAGAAGAAGTGG 1741

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550 CGTTTGATGAAAGATTTGGGCTTGAAGACCCCAGAAGATGACATATGCAAGTATGATTTTG 609
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                                                                                          Example 8; Fig 1; 140pp; English
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97.7%;
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Matches 2059; Conservative
WPI; 2000-587437/55.
           P-PSDB; AAB19578
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                                                                                                  CTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTTAAATATATCTATTTTTACC
                                                                                                                                                       <u> AAAGGTATTTAATATTCTTTTTTATGACAACTTAGATCAACTATTTTTAGCTTGGTAAAT</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRO200; vascular epithelial growth factor E; VEGF-E; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human PRO200 (VEGF-E) cDNA clone DNA29101-1272
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Kuo SS, La Fleur M, 1
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285..1322
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The present sequence is that of cDNA clone DNA29101-1272 or UNQ174 (ATCC 20963) isolated from a human glioma cell line G61 cDNA library using probes (see AAA88523-26) based on an expressed sequence tag (see AAA88522) identified on the basis of homology to vascular endothelial growth factor (VEGF). The clone contains a single open reading frame encoding a 345-amino acid protein (see AAAB19578) and esignated PRO200 or VEGF-B. The isolated cDNA can be used in the recombinant production of PRO200 (VEGF-B). The invention relates to the use of PRO polypeptides, including PRO200, to delay, prevent or rescue retinal cells such as retinal neurons selected from cells, amacrine cells, displaced amacrine cells, displaced amacrine cells, horizontal and bipolar neurons, and supportive cells (including Mueller cells and bipolar neurons, and supportive cells (including Mueller cells including expected by retinal injury, light or environmental trauma or degeneration, including age-related, retinal detachment, retinal teams, retinal degeneration, including age-related, retinal detachment, retinal teams, retinal degenerative myopia, acute retinal neurosis syndrome, traumatic chorioretinapathies or contusion such as Puttscher's retinopathy.
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Novel PRO polypeptides useful for preventing or rescuing retinal cells
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                                from injury caused by ocular diseases such as retinitis pigmentosa, retinopathy, retinal degenerative diseases, degenerative myopia,
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Mermatological; antiarthritic; antirheumatic; immunosuppressive;

Macmatological; antiathoroid; antidabetic; nootropic; neuroprotective;

Mantianaemic; hepatotropic; virudide; antipsoriatic; antialergic;

antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;

missthmatic; systemic lupus erythematosus; rheumatoid arthritis;

Midopathic inflammatory myopathy; systemic sclerosis; sarcoidsis;

Midopathic inflammatory myopathy; systemic maemia; diabetes mellitus;

autoimmune thrombocytopaenia; immune-mediated renal disease;

Memyelinating disease; phepatoblilary disease; Mihipple's disease;

minlammatory bowel disease; gluten-sensitive enteropathy;

autoimmune disease; immune-mediated skin disease; allergic disease;

mununological disease; transplantation associated disease;

my graft rejection; graft-versus-host-disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1930 ATTTAGAAGAAGAACTACATTCATGGTTTGGAAGAGATAAACCTGAAAAGAAGAGTGG 1989
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AGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAATTAA 1621
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                                             1810 AGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTIGCTATGAATTAA
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                                                                                                                                                                                             ACTIGICITATIBATIAGGACAGACIGGATITITICATATITICITATITATITICIGCC
                                                                                                                                                                                                                                                                                    ACTIGIGICATGCIGATAGGACAGACIGGATTTTTCATATTTCTTATTAAAATTTCTGCC
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99WO-US28564.
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04-MAY-1999;
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## (GETH ) GENENTECH INC.

P, Goddard A, Gurney AL, Hebert C, Henzel W; an J, Pennica D, Shelton DL, Smith V; Watanabe CK, Wood WI, Yan M; Baker KP, Goddard A, Lu Y, Pan J, Pennica Ashkenar. Kabakoff RC, Lu x, -+ TA, Tumas D, Ashkenazi AJ,

## WPI; 2000-572271/53. P-PSDB; AAB33414.

Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus

## Claim 23; Fig 1; 309pp; English.

The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, 3jogran's systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombooytopaenia, thyroidits, diabetes mellitus, immune-mediated renal disease, hepatobiliary diseases of the central and peripheral nervous systems, hepatobiliary diseases, inflammatory on peripheral nervous systems, hepatobiliary diseases, inflammatory of immune or immune-mediated skin diseases, allergic diseases, autoimmune or immune-mediated skin diseases, allergic diseases, including agarfic rejection and graft-versus-host-disease.

Immunological diseases of the lung, and transplantation associated diseases including araft rejection and graft-versus-host-disease.

AAC58377 to AAC58378 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAC58579 to AAC58422 and

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TTGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACA 1029
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                                                                                                                              11; Gaps
AAB33414 to AAB33477 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
                                                                                          DB 21; Length 2849;
                                                                                                                              1; Mismatches 36; Indels
                                                         Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;
                                                                                          Score 1979.4;
Pred. No. 0;
                                                                                        Query Match 93.9%;
Best Local Similarity 97.7%;
Matches 2059; Conservative
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Human, PRO, promotion; inhibition; angiogenesis; cardiovascularisation; diagnosis; trauma, wound; cancer; atherosclerosis; cardiac hypertrophy; angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic; cytostatic; gene therapy; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorder in mammals by modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gerber H, Hillan KJ, Goddard A;
Kuo SS, Paoni NF, Smith V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or
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                                                                                                                                                                                                                                          Human PRO713 cDNA sequence SEQ ID NO:136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ferrara N,
Klein RD,
, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            angiogenic disorders in mammals -
                                                                                                                                                  BP
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                                                                                                                                                   standard; cDNA; 2849
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Gurney AL, Kl
Williams PM,
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                  TGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGAGCACACAGGAGGATAGCCGCATC
                                                                                                                                       ACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGGCTGGTTCTATTAGAGAACGT
                                                                                                                                                                              ATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGAT
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angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCB) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB2488 to AAB24435 represent nucleotide and protein sequences used in the exemplification of the present invention.

1090 TITICIGGCCAGGIIGICICCCCGGTIAAACGCTGTGGAAACTGTGCCTGTTGTCTCC 1149 5 970 TIGGAAGAAAAICCAGAGIGGAICHGAACCTICTAACAGAGGAGGAAGAITAIACA 1029 1030 GCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCA 1089 699 481 TACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAAT 729 541 730 ATTITICCTICIGAACCAGGGTICIGCAICCACTACAACATIGICAIGCCACAATICACAG 789 601 849 661 CTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGATGGC 909 721 910 AGTIGGACITAGAAGAICTATATAGGCCAACTIGGCAACTICTIGGCAAGGCTITIGITT 969 TTGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACA 781 GCTGCACACCTCGTAACTTCTCAGTGTCCCATAAGGGAAGAACTAAAGAGAACCGATACCA 841 TITICIGGCCAGGITGICTCCTGGTTAAACGCTGTGGGAACTGTGCCCTGTTGTCTCC 901 GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACTTA 301 549 361 550 cerricardaadarrredecrreaadacceagaadargacararedeadararrarric 609 TAGAAGTTGAGGAACCCAGTGATGGAACTATATTAGGGCGCTGGTGGTTCTGGTACTG 421 310 TGACATCTGCCCTGGCCGGGGGACAGGGGACTCAGGCGGAATCCAACCTGAGTAGTA 369 TTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCAA 241 62 TGACATCTGCCCTGGCCGGCCAGAGACGAGGACTCAGGCGGAATCCAACCTGAGTAGTA 121 AATTCCAGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAA 181 2 cececegradagerereaceceagreagecaaargageererreagerreege 61 490 GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAACTTA CGTTTGATGAAGATTTGGGCTTGAAGACCCCAGAAGATGACATATGCAAGTATGATTTTG TAGAAGTIGAGGAACCCAGTGAAACTATATAGGGCGCTGGTGTGTTCTGGTACTG TACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAAT ATTTTCCTTCTGAACCAGGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCACAG AAGCTGTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATG AAGCTGTGAGTCCTTCAGTGCTACCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATG CTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGATGGC AGTIGGACTITAGAAGAICTATATAGGCCAACTIGGCAACTICTIGGCAAGGTITITIGITT 11; Gaps Query Match
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2059; Conservative 1; Mismatches 36; Indels 11; Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other; 362 250 242 610 422 670 542 790 602 850 722 782 842 122 182 302 482 662 셤 qq ò ð g ò g ð ద Š 임 g à В 셤 ò g ð d qq à ద ò ò g 8888888888 ð 8

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                                             tririaaaaakorgaarr---Ggaaragaarrggragri----Gcaaagacriririgaaaa 2338
                                                                                                                                                                                                   Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate, cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy; ss.
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                           TTTTAAAAAACCTGAATTGGGAANGGAANTTGGTAAGGTTGGCCAAANCTTTTTGAAAA
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Goddard A, Godowski PJ, Gurney AL, Sherwood S;
art TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                                                    Human cDNA sequence encoding for PRO200 polypeptide.
                                                                                                                              AAS21386 standard; cDNA; 2849 BP.
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01-MAR-2000; 2000WO-US05601.

21-MAR-2000; 2000WO-US07377.

21-MAR-2000; 2000WO-US07832.

30-MAR-2000; 2000WO-US13705.

22-MAY-2000; 2000WO-US14042.

30-MAY-2000; 2000WO-US14941.

02-JUN-2000; 2000WO-US15264.
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Gerritsen ME, Goddard
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THE PRO POLYPEPTIGES. The PRO polypeptides are useful to detect other. PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TMF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation of chondrocytes, the proliferation of articular supporting cells of a cytokine from peripheral blood of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide concludes involved in binding interactions. The polymucleotides encoding PRO polypeptides can be used in assays to identify PRO polypeptides can be used to assays to identify PRO polypeptides can be used to assays to identify PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
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other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical
                                                                                                                                                                                                                                                                                                 AAS21244-AAS21518 encode for novel human secretory and transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1979.4; DB 22; Length 2849;
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Matches 2059; Conservative 1; Mismatches
                                                                                                                                                                                                           Claim 3; Fig 285; 813pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                       The present sequence is one of seventeen nucleic acids encoding PRO polypeptides. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating cardiovascular, endothelial or angiogenic disorders in a mammal. Examples of these disorders include cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atheroscelerosis, hypertension, arterial restenoiss, Raymaud's disease, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and antagonists are also used to prevent tumour angiogenesis and for treating periodonial diseases. They are also used to stimulate wound healing and tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO antibodies are useful for diagnosing a cardiovascular, endothelial or angiogenic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGACATCTGCCCTGGCCGGCCAGAGACGAGGGACTCAGGCGGAATCCAACCTGAGTA
                                                                                                                                                                                              Seventeen nucleic acids encoding PRO polypeptides which are useful in diagnosis and treatment of cardiovascular, endothelial or angiogenic disorders.in a mammal -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTGG
                                                                                              Marsters SA;
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Pred. No. 0;
                                                                                Gerritsen ME;
                                                                           Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen
Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Ma
Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36; Indels
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Best Local Similarity 97.7%;
Matches 2059; Conservative
21-MAR-2000; 2000WO-US07532.
30-MAR-2000; 2000WO-US08439.
                                                  (GETH ) GENENTECH INC.
                                                                                                                                               WPI; 2001-025251/03.
                                                                                                                                                                  P-PSDB; AAB50952
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1622 ACTTGTGTCRTGCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAAATTTCTGCC 1681 1262 1322 1570 1442 1502 1202 1382 ద g ò g ò 셤 ò 8 음 à ద ð 셤 ð 유 ò 369 549 609 729 429 241 489 301 361 421 699 481 541 730 ATTITCTICIGAACCAGGGTICIGCATCCACCAACATIGICATGCCACCAACAGG 789 181 TGACATCTGCCCTGGCCGGCCAGAGAGAGAGCTCAGGCGGAATCCAACCTGAGTA TTATTACTGTGTGTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCAA TTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCAA GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACTTA certricardaaacartricescriteaaceceacaacarcarariceacararararrire TAGAAGTTGAGGAACCCAGTGATGGAACTATATTAGGGCGCTGGTGTGGTTCTGGTACTG TACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAAT ATTITICCTICTGAACCAGGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCACAG AATTCCAGTTTTCCAGCAACAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAAA 370 AATTCCAGTTTTCCAGCAACAACAACAGACGGAGTACAAGATCCTCAGCATGAGAA GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGAAAATGTATGGATACAACTTA CGTTTGATGAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATTTTG 362 610 182 242 302 550 422

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                                                                                                                                                                                                               TITICTAAACACAATIGITATAGCCAGAGGAACAAAGAIGGATATAAAAATATIGITGCC 1981
                                                                                                                                                                                                                                                          1982 CTGGACAAAATACATGTATNTCCATCCCGGAATGGTGCTAGAGTTGGATTAAACCTGCA 2041
                                                                                                                                                                                                                                                                               227 TCTGACAAAATACATGTATTT-CATTCTGGTATGGTGCTAGAGTTAGATT-AATCTGCA 2284
                                                                                                                                                                                                                                                                                                                    1870 ACTIGIGICALGATAGGACAGACTGGATTTTTCATATTATTATAAAATTTCTGCC 1929
                                                                                                    2049
                                                                                                                         CTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTTAAATATATTTTTTACC 1861
                                                                                                                                                                    1921
                                                                                                                                                                                                                                                                                                    TITIAAAAAACCIGAAITGGGAANGGAANTIGGIAAGGIIGGCCAAANCTITITIGAAAA 2101
                                                                               1801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; PRO526; PRO719; PRO200; PRO725; PRO1031; immune related disease; inflammation; thyroiditis; demyelinating disease; skin disease; infectious disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New compositions containing a PRO526, PRO719, PRO725, PRO1031 or PRO200 proteins for modulating immune response or proliferation of T-lymphocytes in mammal, especially for treating immune related disorders, e.g. graft rejection -
                                               ATTTAGAAGAAGAAGAACTACATTCATGGTTTGGAAGAGATAAACCTGAAAAGAAGAGTGG
                                                                                                                                                                     AAAGGTATTTAATATTCTTTTTTATGACAACTTAGATCAACTATTTTTAGCTTGGTAAAT
                                   <u> ATTTTAGAAGAAGAACTACATTCATGGTTTGGAAGAGATAAACCTGAAAAGAAGAGTGG</u>
                                                                                CCTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTTCATTGTGTGTACATTTTTATATT
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Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                             AAC88962 standard; cDNA; 2849 BP.
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Tumas D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human PRO200 coding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                      TAATTAA 2345
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Kuo SS,
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                                                                                        The present invention discloses the coding and protein sequences of human
                                                                                                                             proteins PRO526, PRO719, PRO725, PRO1031 and PRO200. These proteins, their coding sequences and antibodies can be used in the treatment of immune-related diseases, including systemic lupus erythematosus, rheumatoid arthritis, thyroiditis, immune-mediated renal disease, demyelinating diseases such as multiple sclerosis, hepatobiliary diseases including primary biliary cirrhosis, inflammatory bowel diseases, including asthma, immunologic diseases of the lung, transplantation associated diseases and infectious diseases such as RIV and hepatitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 0;
1; Mismatches
Claim 21; Fig 9; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 93.9%;
Best Local Similarity 97.7%;
Matches 2059; Conservative 1
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                                                                                                     CTGGACAAAAATACATGTATNTCCATCCCGGAATGGTGCTAGAGTTGGATTAAACCTGCA
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... MR, Marsters SA;
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or
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AL, Hillan KJ, Kuo SS, Mark MR, M:
Watanabe CK, Williams PM, Wood WI;
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Claim 58; Fig 21A-B; 293pp; English.

The invention relaters to mover numen amiglogenesis-sassolated proceins designated PRO proteins (AAB53064-BE3097), and to nucleic acids encoding PRO proteins. The invention also relates to vectors and host cells PRO protein, PRO antibodies specific for a PRO protein, fusion proteins comprising a PRO nucleic acid, the recombinant production of a PRO protein, PRO antibodies specific for a PRO protein, fusion proteins compounds which inhibit the expression of a PRO gene. The invention additionally encompasses methods of identifying modulators of PRO expression or activity; diagnosing a cardiovascular. Endothelial or angiogenic disorder, or a Busceptibility to such a disorder by detecting mutations in a PRO gene, or the expression level of a PRO gene within a particular tissue; treating a cardiovascular, endothelial or proteins are are proposed via the administration of a PRO protein, PRO nucleic acid, or PRO agonist or antagonist; a retroviral gene therapy vector comprising or PRO mucleic acid, and methods of inhibiting or stimulating endothelial coll growth, cardiac Hypertrophy or PRO-induced angiogenesis via the administration of a PRO protein, and agonist or an agonist or antagonist thereof or appearance acids, PRO proteins, antibodies against PRO proteins, PRO appearance acids, proporteins, antibodies against PRO proteins, proposition of a production of a proposition of a production of a production of a proposition of a production of a production of a production of a product invention relates to novel human angiogenesis-associated proteins protein of the invention.

Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;

121 369 181 609 421 699 CCCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTGC 309 429 430 Tratracreretratratrecandratreacadeceaagerreceratatrarecaa 489 301 361 481 670 TACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAAT 729 CCCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTGG TGACATCTGCCCTGGCCGGCCAGAGACGAGGACTCAGGCGGGAATCCAACCTGAGTAGTA AATTCCAGTTTTCCAGCAACAAGAACAGAACGGAGTACAAGATCCTCAGCATGAGAAA GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGGAAAAATGTATGGATACAACTTA CGTTTGATGAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATTTTG 610 TAGAAGTIGAGGAACCCAGIGAIGGAACIATATAAGGCCGCTGGIGGGTTCTGGTACTG TACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAAT 310 reacarcreceredecedededededededededededaarccaaccreagragra 370 AATTCCAGTTTTCCAGCAACAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAAA 242 GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACTTA 550 CETTIGAIGAAGAITIGGGCTIGAAGACCCAGAAGAIGACAIAIGCAAGIAICAITIIG TAGAAGTTGAGGAACCCAGTGATGGAACTATATTAGGGCGCTGGTGTGGTTCTGGTACTG TTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCAA 11; Gaps Score 1979.4; DB 22; Length 2849; Pred. No. 0; 1; Mismatches 36; Indels 11; C 93.9%; ilarity 97.7%; Conservative Query Match Best Local Similarity Matches 2059; ~ 122 490 302 62 P a gg 요 셤 à ò 8 8 ð g ò 셤 8 à

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29-JUN-2001; 2001WO-US21066.
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14-MAY-1999;
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1622 ACTIGIGICRIGCIGATAGGACAGACTGGATTITICATATTICTTATTAAAATITCTGC 1681
                                         1870 ACTTGTGTCATGCTGATAGGACAGACTGGATTTTTCATATTATTAATAAATTTCTGCC 1929
                                                                        1682 ATTTAGAAGAAGAGAACTACATTCATGGTTTGGAAGAGATAAACCTGAAAAGAGAGTGG 1741
                                                                                   1930 ATTTAGAAGAAGAACTACATTCATGGTTTGGAAGAGATAAACCTGAAAAGAAGAGTGG 1989
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                                                                                                                                                                                                                                                                               1982 CTGGACAAAAAACATGTATNTCCATCCCGGAATGGTGCTAGAGTTGGATTAAACCTGCA
                                                                                                                                                                                                                                                                                                                       TTTTAAAAAACCTGAATTGGGAANGGAANTTGGTAAGGTTGGCCAAANCTTTTTGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; PRO polypeptide; secreted and transmembrane protein; tumour necrosis factor-alpha; TNF-alpha; blood; proliferation; differentiation; chondrocyte; tumour; genetic disorder; cytostatic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding human PRO polypeptide #143.
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98WO-US14556.
98WO-US17888.
98WO-US18824.
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98WO-US19093.
98WO-US19177.
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430 TIATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCAA 489

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New secreted and transmembrane PRO nucleic acids, useful for gene therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in chromosome identification
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                                                                                                                                                                                                                                                               Claim 2; Fig 285; 660pp; English.
      2001US-0854208.
2001US-0854280.
2001US-0850216.
2001US-0866024.
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19-DEC-2001; 2001US-0028072.
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Smith V, Stewart TA, Tum
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                                                                                                                                                (GETH ) GENENTECH INC.
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1150 ACAATTGCAATGAATGTCAATGTGTGCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCC 1209 970 TTGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACA 1029 1030 GCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGGAAACGGATACCA 1089 1090 irrircitedecidesinsiciteciderridakeserisisensesakersiseeersinsieretee 1149 1390 ATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGAT 1449 1022 TGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGAGCACACAGGAGGATAGCCGCATC 1081 TTACAGTGCATTCTGAAAGAGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTT 1261 1450 miacagrocarrendaagagagagacarcaaacagaarraggagrocgacacagcrerr 1509 490 GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACTTA 549 842 TTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACTGTGCCTGTTGTCTCC 901 670 TACCAGGAAAACAGTTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAAT 729 610 TAGAAGTTGAGGAACCCAGTGAAGTAATTAAGGGCGCTGGTGGTTCTGGTACTG ATTTTCCTTCTGAACCAGGGTTCTGCATCCACTACAACATGTCATGCCACAATTCACAG 790 AAGCIGIGAGICCTICAGIGCTACCCCCTICAGCTTIGCCACTGGACCTGATAATG GAAATACGGTCTTGGTATGGAGTTAGTAGCAGTAGAGGAAAATGTATGGATACAACTTA CGTTTGATGAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATTTTG <u> ATTTTCCTTCTGAACCAGGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCACAG</u> 542 AAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATG 910 AGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTTT 782 GCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCA TAGAAGTTGAGGAACCCAGTGATGGAACTATATAGGGCGCTGGTGTGGTTCTGGTACTG <u>TACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGAAGAT</u> CTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGATGGC 850 craraacigccirragracciridgaagaccirarricgararcirigaaccagagargcc AGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTTT TTGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACA 902 ACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCC 1142 ATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGAT 362 730 662 1202 1262 302 422 482 602 962 ઠે 셤 ద g 셤 à ద ద ð 쉽 à 셤 셤 셤 à ď ઠે d Š ద Š g ò 셤 ઠે g ð à ò 엄 ò පි ò The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for linking bioactive molecules to cells expressing PRO polypeptides, for linking bioactive molecules to cells expressing PRO polypeptides, and for for identifying agonists or antagonists.

The PRO polypeptides are useful for for stimulating the release of tumour necrosis factor (TNF)-alpha from human blood, for stimulating the proliferation or differentiation of chondrocytes, and detecting the proliferation or differentiation of chondrocytes, and detecting the presence of tumours. The polynuclectide sequences encoding PRO polypeptides, in the generation of stimulating transgenic animals or knockout animals, for the genetic analysis of individuals with genetic disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs encoding the human PRO polypeptides of the invention.

Note: The sequence data for this patent was obtained in electronic formals. 250 coccocidadicacororox coccadioacca and analox controca 121 AATTCCAGTTTTCCAGCAACAAGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAA 181 370 AATTCCAGTTTTCCAGCAACAAGGAACAGGAGTACAAGATCCTCAGCATGAGAA 429 TTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCAA 241 Filvaroff E, Gao W; 2 CCCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCAAATGAGCCTCTTCGGGCCTTCTCCTGG 62 TGACATCTGCCCTGGCCGGCCAGAGACGAGGGACTCAGGCGGAATCCAACCTGAGTAGTA 36; Indels 11; Gaps DeForge L, Desnoyers L, Filvaroff E, G. A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; Score 1979.4; DB 25; Length 2849; Query Match 93.9%; Score 1979.4; Best Local Similarity 97.7%; Pred. No. 0; Matches 2059; Conservative 1; Mismatches 122

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1930 ATTTAGAAGAAGAACTACATTCATGGTTTGGAAGAGATAAACCTGAAAAGAAGAAGTGG 1989
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                                                                  1570 TIGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGGTGG 1629
                                                                                                                                                                            GTICTOTATITICAGITOTITICGATACGGCTTAGGGTAAIGTCAGTACAGGAAAAAACTG 1441
                                                                                                                                                                                                                                                  1630 GITCIGIAITICAGITCITICGATACGGCTTAGGGTAATGICAGTACAGGAAAAAAACTG 1689
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                               TIGIAITAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGG 1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2170 TITTCTAAACACAATIGTTATAGCCAGAGGAACAAAGATG---ATATAAAATATIGTIGC
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                                                                                                                                                                                                                                                                                                                         1442 IGCAAGTGAGCACCTGATTCCGTTGCCTTAACTCTAAAGCTCCATGTCCTGGGCCT
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AC ACRO4
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02-MAR-2000; 2000MO-US05546.

02-MAR-2000; 2000MO-US05641.

10-MAR-2000; 2000MO-US06884.

15-MAR-2000; 2000MO-US06884.

21-MAR-2000; 2000MO-US07377.

21-MAR-2000; 2000MO-US07532.

30-MAR-2000; 2000MO-US08439.

17-MAR-2000; 2000MO-US08439.

22-MAR-2000; 2000MO-US1705.

22-MAR-2000; 2000MO-US14941.
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US2003032155-A1
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from any of the nucleotide sequences cited above. The nucleic acids and polypeptides are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or diabetic complications. The nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing.

The present sequence encodes a PRO protein of the invention.

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The invention relates to an isolated mucleic acid comprising, or which is at least 80% identical to, or the full-length coding sequence of, any of the 275 mucleotide sequences, encoding the corresponding PRO polypeptide (one of 275 secreted or transmembrane proteins). The mucleic acid by polypeptide (nome of 275 secreted or transmembrane proteins). The mucleic acid caid or turber comprises the full-length coding sequence of the DNA deposited under American Type Chilture Collection (ATC) accession number in a list given in the specification. Also included are vectors and host cells for producing PRO proteins, PRO fusion proteins, methods are vectors and host cells for producing PRO proteins, methods for simulating the release of TNP-alpha (tumour necrosis factor alpha) from human blood,

TNP-alpha (tumour of endothelial cells), a method for modulating the release or profiferation of endothelial cells), a method for modulating the uptake of ground for inhibiting the binding of A-peptide to factor VIIA,

TNP-alpha (tumour in a mammal and an oligonucleotide probe derived) Beresini M, ME, Goddard (GETH ) GENENTECH INC. Stewart TA, WPI; 2003-331925/31. P-PSDB; ABU66988. 29-JUN-2001) 09-JUN-2001) 28-DEC-2000) 28-FEB-2001) 09-MAR-2001) 22-MAR-2001) 25-APR-2001) 10-MAY-2001; 18-MAY-2001; 25-MAY-2001; Ξ 01-DEC-2000; 20-DEC-2000; 28-FEB-2001; 25-MAY-2001; 01-JUN-2001; 21-JUN-2001; 18-JUL-2001; 06-AUG-2001; 20-JUN-2001; 19-JUN-2001; 24-AUG-2000; 08-NOV-2000; 14-JUN-2001; Eaker KP, Gerritsen Smith V, 

2001US-09796498. 2001US-0802706. 2001US-080E89. 2001US-081E744. 2001US-0854209. 2001US-0854200. 2001US-0854280. 2001US-0866034. 2001US-0872035. 2001US-0874503. 2001US-0882636. 2001US-0887879 2001US-0908827 2001US-0924419. 19-DEC-2001; 2001US-0028072 2000US-0747259

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429 241 489 301 549 361

310 reacarcrecocredecedeceadacadedecededecedaarccaaccreacradra 369

TGACATCTGCCCTGGCCGGCCAGAGGACGAGGGACTCAGGCGGAATCCAACCTGAGTAGTA

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370 AATTCCAGTTTTCCAGCAACAAGAACAGAACGGAGTACAAGATCCTCAGCATGAGAAA

TTATTACTGTGTCTACTAATGGAAGTATTCACAGGCCCAAGGTTTCCTCATACTTATCCAA GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACTTA

182 430 242 490 302

GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAAGGAAAATGTATGGATACAACTTA

AATTCCAGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAA

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250 CCCGCCGTGAGTGAGCTCTCACCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCGC 309

2 CCCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCCAAATGAGCCTCTTCGGGCTTCTCTCTGG

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Query Match 93.9%; Score 1979.4; DB 25; Length 2849; Best Local Similarity 97.7%; Pred. No. 0; Matches 2059; Conservative 1; Mismatches 36; Indels 11; (

Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;

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36; Indels 11; Gaps

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421

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481 729 541 789

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661 909

Gao W; DeForge L, Desnoyers L, Filvaroff E, G: A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or cancer

Claim 2; Fig 285; 659pp; English.

970 TTGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACA 1029 1030 GCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAAGAACCGATACCA 1089 790 AAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATG 849 910 AGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTTT 969 TIGGAAGAAATCCAGAGIGGIGGAICTGAACCTICIAACAGAGGAGGIAAGAITAIACA 781 AGTIGGACTIAGAAGAICTATATAGGCCAACTIGGCAACTICTIGGCAAGGCTTTIGTTT 721 TTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACTGTGCCCTGTTGTCTCC 901 550 CGTTTGATGAAGATTTGGGCTTGAAGACCCCAGAAGATGACATATGCAAGTATGATTTTG TAGAAGTTGAGGAACCCAGTGATGGAACTATATTAGGGCGCTGGTGTGGTTCTGGTACTG 610 TAGAAGTTGAGGAACCCAGTGATGGAACTATATTAGGGCGCTGGTGGTGTGTTCTGGTACTG 670 TACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAAT ATTITICCTTCTGAACCAGGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCACAG 730 ATTTTCCTTCTGAACCAGGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCACAG AAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATG CTATAACTGCCTTTAGTACCTTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGATGGC CTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGACGCC **TACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAAT** 362 422 482 542 602 850 662 722 782 842 d 셤 ð ద ð 임 ò 셤 ਨੇ ð 셤 ò ద ઠે 셤 ò 셤 ò

Db 2170 TTTCTAAACACAATTGTTATAGCCAGAGGAAC Qy 1982 CTGGACAAAAATACATGTATATCCATCCGGAA	2227		Db 2339 TAATTAA 2345	Search completed: November 26, 2003, 00:11:25 Job time : 398.226 secs														
	902 ACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCC 961 	962 ITCAGITGAGACCAAAGACGGGTGICAGGGGATIGCACAAAICACICACGGACGIGGCCC 1021 	1022 TGGAGCACCATGAGGAGTGTGACTGTGTGTAGAGGAGCACAGGAGGATAGCCGCATC 1081 	1082 ACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCCTGATTCTATTAGAGAACGT 1141	1142 ATGOGITARCICCATCCATAATCICAGATGITTGCTTCAAGACCITTCATCTTCAGGAT 1201 	1202 TTACAGTGCATTCTGAAAGAGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTT 1261 	1262 TTGAGAGGGCCTAAAGGACAGGAAAAGGTCTTCAATCGTGGAAAGAAA	1322 TIGTATTAAATAGAFCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGG 1381 	1382 GITCIGIAITICAGITCITICGAIACGGCITAGGGIAAICICAGIACAGGAAAAAACIG 1441 	1442 IGCAAGIGAGCACCIGAITCCGITGCCTTGCTTAACICTAAAGCTCCATGTCCTGGGCCT 1501 	1502 AAAAFCGTAJAAAAFCTGGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	1562 AGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAATTAA 1621 	1622 ACTIGIGICRIGCIGAIAGGACAGACIGGATITICAIAITICTIAITAAAAITICIGCC 1681 	1682 ATTTAGAAGAAGAACTACATTCATGGTTTGGAAGATAAACCTGAAAAGAAGAGGTGG 1741 	1742 CCTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTTATATT 1801 	1802 CICCITITGACAITAIAACIGIIGGGIITICIAAICIIGITAAAIAIAICIAITITIACC 1861 	1862 AAAGGTATTAAATATTCTTTTTATGACAACTTACATCAACTATTTTTAGCTTGGTAAAT 1921 	1922 TITICIAAACACAAITGITAIAGCCAGAGGAACAAAGAIGIGAAAAAAATAITGITGCC 1981

2226	2041	2284	2101	2338		
2170 TITICIAAACACAATIGITATAGCCAGAGGAACAAAGAIGAIATAAAATATTGTIGC 2226	1982 CTGGACAAAATACATGTATNTCCATCCCGGAATGGTGCTAGAGTTGGATTAAACCTGCA 2041	2227 TCTGACAAAAAATACATGTATTT-CATTCTCGTATGGTGCTAGAGTTAGATT-AATCTGCA 2284	TTTTAAAAAACCTGAATTGGGAANGGAANTTGGTAAGGTTGGCCAAANCTTTTTTGAAAA 2101	TTTTAAAAACTGAATTGGAATAGAAT	2102 TAATTAA 2108	2339 TAATTAA 2345
2170	1982	2227	2042	2285	2102	2339
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'GGTZ 6/ptodata/2/ina/5A_COMB.seq:*
'CGTZ 6/ptodata/2/ina/5B_COMB.seq:*
'GGTZ 6/ptodata/2/ina/6A_COMB.seq:*
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'CGTZ 6/ptodata/2/ina/PCTUS COMB.seq:*
'CGTZ 6/ptodata/2/ina/PCTUS COMB.seq:*
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## s2, Appl 1, Appli 1, Appli Sequence 13, Appl Sequence 288, App Sequence 230, App Sequence 32, Appl Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1137, Sequence 89, 7 Seguence 36, Sequence 36, Sequence 1, 1 Sequence 1, Sequence 50, Sequence 13 Sequence 42 Sequence 34 Description Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seguence Sequence US-09-040-220D-1 US-09-265-686-1 US-09-706-968-1 US-09-457-066-1 US-09-457-066-1 US-09-457-066-1 US-09-564-59D-34 US-09-564-59D-34 US-09-564-59D-6 US-09-457-066-4 US-09-457-066-4 US-09-457-066-4 US-09-564-59D-6 US-09-564-59D-1 US-09-564-59D-1 US-09-564-59D-1 US-09-564-59D-1 US-09-564-59D-1 US-09-564-59D-1 US-09-966-36 US-08-98 SUMMARIES Query Match Length DB 636 1342 1664976 777.1 76.4 47.2 47.2 45.5 45.5 34.8 1624.8 1624.8 994.8 994.8 959.4 959.4 734.4 177.6 117.8 117.8 49.2 48.8 47.8 Score 102.8 55.2 52.2 50.4 1624.8 Result υυ U

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Sequence 5, Appli Sequence 1, Appli	Sequence 1, Appli Sequence 7, Appli	Sequence 6, Appli Sequence 8, Appli	Sequence 8, Appli	14,	151,	Sequence 95, Appl	Sequence 5, Appli	Sequence 1, Appli	Sequence 534, App	Sequence 287, App	Sequence 1, Appli	Sequence 3, Appli	Sequence 191, App
US-09-417-485D-5 US-08-446-855A-1	US-09-150-741-1 US-09-417-485D-7	US-08-628-417-6 US-08-300-903A-8	US-08-988-197-8	US-09-014-969-14	US-09-370-838-151	US-09-602-877A-95	US-09-417-485D-5	US-08-947-823-1	US-08-998-416-534	US-08-998-416-287	US-09-835-811-1	US-09-801-861-3	US-08-998-416-191
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## ALIGNMENTS

RESULT 1 US-09-040-220D-1

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APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
APPLICANT: Kuo, Sophia S.
TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR
TITLE OF INVENTION: REDOTHELIAL CELL GROWTH FACTOR AND BONE MORPHOGENETIC
TITLE OF INVENTION: PROTEIN 1 AND NUCLEIC ACIDS ENCODING SAME, THEIR USES,
TITLE OF INVENTION: AND PROCESSES FOR THEIR PRODUCTION
FILE REPRENCE: P11.2
CURRENT APPLICATION NUMBER: US/09/040,220D
CURRENT PILING DATE: 1998-03-17
NUMBER OF SEQ ID NOS: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284 TGACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTAGTA 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     404 TIAITACTGRGICTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCAA 463
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OTHER INFORMATION: N is A, T, C or G
; Sequence 1, Application US/09040220D
; Patent No. 6391311
; GENERAL INFORMATION:
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Matches 2059; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 2825
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Db 1604 GTTCTGTATTTCAGTTCTTTCGATACGGCTTAGGGTAAT	1664	Db 1724 AAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTTT	Qy 1562 AGAACATICTAIGIACTACAAACCIGGTITITAAAAAGG Db 1784 AGAACATICTAIGTACTACAAACCIGGTITITAAAAAG	1622	1682 A 1904 A	1964	2024	2084	1922	1982 C 2201 T	2042	Cy 2102 TAATTAA 2108 Db 2313 TAATTAA 2319	RESULT 2 US-09-265-686-1 ; Sequence 1, Application US/09265686	í E	; TILE OF LAVENILON: POLITEETIDES HOMOLOGOUS TO VI ; FILE REFERENCE: P112222 ; CURRENT APPLICATION NUMBER: US/09/265,686 ; CURRENT FILING DATE: 1999-03-10	; PRIOR APPLICATION NOMBER: US 09/040,220 ; PRIOR FILING DATE: 1998-03-17 ; PRIOR APPLICATION NUMBER: US 09/184,216 ; PRIOR FILING DATE: 1998-11-02	; SRQ ID NOS: 8 ; SRQ ID NO 1 ; LENGITH: 2825 ; TYPE: DNA	; ORGANISM: Human ; FEATURE: ; NAME/KEY: Unknown
Con recommendations to the contract of the con	<b>ს</b> — ს	422 TACCAGGAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAAT 481 	ATTITCCTTCTGAACCAGGGTTCT	AAGCTGTGAGTCCTTCAGTGCTAC	602 CTATAACTGCCTTTAGTACCTTGGAAGACCTTATTGGATATCTTGAACCAGAGAGAG	662 AGTIGGACTIAGAAGAICTAIATAGGCCAACTIGGCAACTICTIGGCAAGGCTITIGIFT 721 	722 TIGGAAGAAATCCAGAGTGGGATCTGAACCTTCTAACAGAGGGGGAAGTTATACA 781 	782 GCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAAACGATACCA 841 	842 TITICIGGCCAGGIIGICTCCIGGIIAAAGGCIGIGGGAAACIGIGCCIGIIGICCC 901 	902 ACAATTGCAATGAATGTCAATGTGTCCCAAAGATAACTAAAAAAATACACGGGGTCC 961 	962 TTCAGTTGAGACCGAAAGACCGGTGTCAGGGGATTGCACAAAATCACTCAC	1022 TGGAGCACCATGAGGAGTGTGAGACTGTGTGCAGAGGAGCACAGGAGGATAGCCGCATC 1081 	1082 ACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCCAGTTCTATTAGAGAACGT 1141	1142 AIGCGITAICICCAICCTTAAICICAGITGITIGCTICAAGACCITICAICTICAGGAI 1201 	1202 TIACAGTGCALTCTGAAAGAGAGACALCAAACAQAATTAGGAGTTGTGCAACAGCTCTT 1261 	1262 TTGAGAGGAGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAA	1322 TIGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGG 1381 	1382 GTTCTGTAFTTCAGTTCTTTCGATACGCCTAAGGGTAATGTCAGTACAGGAAAAAAACTG 1441
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                                                                                                                                                            224 CCCCCCGAGGCGTCTCACCCCAGTCACCCCAATGAGCCTCTTCGGGCTTCTCCTGC 283
                                                                                                                                                                                                                                 182 TTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCAA 241
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                                                                Query Match 93.9%; Score 1979.4; DB 4; Length 2825; Best Local Similarity 97.7%; Pred. No. 0; Matches 2059; Conservative 1; Mismatches 36; Indels 11;
; LOCATION: 2689
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142 364	ADGOGNTALCTCCATCCTTAATCTCAGTIGTTTGCTTCAAGGACCTTTCATCTTCAGGAT 1201
202	TTACAGTGCATTCTGAAAGAGAACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTT 1261 
262	TTGAGAGGGGCCTAAAGGACAGAGAAAAGGTCTTCAATCGTGGAAAAAAATTAAATG 1321 
(A) 44	MITAARIAGAICACCAGCTAGTITCAGAGTTACCATGTAC 
1382	CAGITCITICGATACGGCTTAGGGAAATGTC 
442	TGCAAGTGAGCACCTGATTCCGTTGCCTTAACTCTAAAGCTCCATGTCCTGGGCCT 1501 
1502	AAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTGCTCATATTCACATATGTAAACC 1561 
1562	AGAACATTCTAIGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAATTAA 1621 
1622 1844	ACTIGIGECRIGGEGARAGACAGACTGGATITITCAIATTGTATTAAAATTTCTGCC 1681 ACTIGIGECATGCTGATAGACAGACTGGATTTTTCCATATTATAAAATTTCTGCC 1903
1682	ATTTAGAAGAAAGTACATTCATGGTTTGGAAGAGATAAACCTGAAAAGAAGAGTGG 1741 
1742	CCTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTTATATT 1801
1802	CTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTTAAATATATCTTTTTTACC 1861
1862	AAAGGTATTTAATATTCTTTTTATGACAACTTAGATCAACTATTTTTAGCTTGGTAAAT 1921 
1922	TTTTCTAAACACAATTGTTATAGCCAGAGGAACAAAGATGGATATAAAAATATTGTTGCC 1981 
1982	CTGGACAAAAATACATGTATNTCCATCCCGGAATGGTGGTTGGATTAAACCTGGA 2041
2201	ATACATGTATTT-CATTCTCGTATGGTGCTAGAGTTAGATT-AATCTG
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1019 ACAATTGCAATGAATGTGTCTCCCAAGCAAAGTTACTAAAAATACCACGAGGTCC 1078
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                                                                                                                                              659 AAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATG 718
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                            599 ATTITICCTICIGAACCAGGGTICTGCATCCACTACAACATTGTCATGCCACAATTCACAG 658
                                                                                        542 AAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATG 601
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ORGANISM: Homo sapiens
                                                                           2102 TAATTAA 2108
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                                                                                                 719 CTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGATGGC 778
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542 AAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATG 601
                                                                                                                                                                      CTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGATGGC 661
                                                                                                                                                                                                                                                                                                                     779 AGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTTT 838
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       1679 CAGAACATTCTATGTACTACAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAATTA 1738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239 AATTCCAGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAA 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 TGACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTAGTA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 AATTCCAGTTTTCCAGCAACAAGAACAGAAGAGAGTACAAGATCCTCAGCATGAGAAA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTAITACTGTGTGTCTACTAATGGAAGTATTCACAGCCCCAAGGTTTCCTCATACTTATCCAA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACTTA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        359 GAAATACGGTCTTGGTATGGAGTTAGTAGCAGTAGGAAAATGTATGGATACAACTTA 418
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77.1%; Score 1624.8; DB 4; Length 1760;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1637; Conservative 1; Mismatches 3; Indels 1;
                                                                                                                                                                                                                                                                                           APPLICANT: Hart, Charles E.
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Glibertson, Debra G.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REFERENCE: 98-6001
CURRENT APPLICATION NUMBER: US/09/706,968
CURRENT FILING DATE: 2000-11-06
PRIOR APPLICATION NUMBER: US/09/541,752
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                        1621 AACTIGIGICRIGCIGATAGGA 1642
                                                                                    1739 AACTIGIGICTCGTGCTGATAGGA 1760
                                                                                                                                                                                                                         Sequence 1, Application US/09706968 Patent No. 6528050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) NAME/KEY: CDS
; LOCATION: (154)...(1191)
US-09-706-968-1
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                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 1
LENGTH: 1760
                                                                                                                                                                                                    US-09-706-968-1
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                      542 AAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATG 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1319 GGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAAT 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACTTA 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGACATCTGCCCTGGCCGGCCAGAGACGAGGACTCAGGCGGAATCCAACCTGAGTAGTA 121
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                                                                                                                                                                                                                                                                   Sequence 1, Application US/09457066;
Fatent No. 6432613
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gao, Zeren
APPLICANT: Piddington, Christopher S.
APPLICANT: Piddington, Christopher S.
APPLICANT: Shoghard, Paul O.
APPLICANT: Shoghard, Paul O.
APPLICANT: Shoghard, Paul O.
APPLICANT: Glibertson, Debra G.
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APPLICANT: GINENTION: GROWTH FACTOR HOMOLOG ZVEGF3;
FILE REFERENCE: 98-60
CURRENT FILING DATE: 1999-12-07;
NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PastSEQ for Windows Version 3.0
                                                                      1621 AACTIGIGICRIGCIGAIAGGA 1642
                                                                                                       1739 AACTTGTGTCGTGCTGATAGGA 1760
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LOCATION: (154)...(1191)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1760
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US-09-457-066-1
                                                                                                                                                                                                                                            RESULT 5
US-09-457-066-1
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977 AGACCGGTGTCAGGGGATTGCACAAATCACTCACCGACGTGGCCCTGGAGCACCATGAGG 1036
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                                                                                                     680 AICTAIAIAGGCCAACTIGGCAACTICTIGGCAAGGCTTTTTGGTTTTTTGGAAGAAAATCCA 739
                                                                                                                                                                                                    860 GTCTCCTGGTTAAACGCTGTGGTGGAACTGTGCCTGTTGTTTCTCCACAATTGCAATGAAT 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          920 GTCAATGTGTCCCAAGCTAAGTTACTAAAAATACCACGAGGTCCTTCAGTGAGACCAA 979
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                                                       677 AICTATATAGGCCAACTIGGCAACTICTIGGCAAGGCTITTGTTTTGGAAGAAAATCCA 736
                                                                                                                                                                                                                                                                                      797 ACTICTCAGIGICCAIAAGGGAAGAACIAAAGAGAGAACCGAIACCAITTICIGGCCAGGII 856
                                                                                                                                                                                                                                                                                                                                                                                                     857 GICTCCTGGTTAAACGCTGTGGGGAACTGTGCCTGTTGTCTCCACAATTGCAATGAAT 916
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620 GTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGATGGCAGTTGGACTTAGAAG 679
                                                                                                                                                                  737 GAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTA 796
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47.2%; Score 994.8; DB 4; Length 1095;
Best Local Similarity 99.8%; Pred. No. 3.8e-244;
Matches 996; Conservative 0; Mismatches 2; Indels 0;
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APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles B.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O.
APPLICANT: Shepmarer, Kimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOWOLOG ZVEGF3
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CURRENT APPLICATION NUMBER: US/09/706,968
CURRENT PILING DATE: 2000-11-06
PRIOR APPLICATION NUMBER: US/09/541,752
PRIOR FILING DATE: 2000-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 50, Application US/09706968
; Patent No. 6528050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 50
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Best Local Similarity 99.8%; Pred. No. 3.8e-244;
Matches 996; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                APPLICANT: Gao, Zeren
APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Piddington, Christopher S.
APPLICANT: APPLICANT: Abnemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION GROWIH FACTOR HOMOLOG ZVEGF3
CURRENT APPLICATION NUMBER: US/09/457,066
CURRENT PILLING DATE: 199-112-07
NUMBER OF SEQ ID NOS: 50
SOPTWARE: FastSEQ for Windows Version 3.0
                                    1739 ATTARACTIGIGICGIGCIGAIAGGA 1764
         1617 ATTAAACTTGTGTCRTGCTGATAGGA 1642
                                                                                                                                                                                             Sequence 50, Application US/09457066
Patent No. 6432673
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                         317 TIGGGCTIGAAGACCCAGAAGATGACATATGCAAGTATGATTTGTAGAAGTIGAGAAC 376
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200 CTAAIGGAAGTAITCACAGCCCAAGGITTCCTCATACTTAICCAAGAAATACGGICTIGG 259
                                                                                     TATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACTTACGTTTGATGAAAGAT 316
                                                                                                                                                                                                                                                                                                                                               3.0 TTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATTTTGTAGAAGTTGAAGAAC 379
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RESULT 8
US-09-564-595D-34

Sequence 34, Application US/09564595D

Sequence 34, Application US/09564595D

Sequence 34, Application US/09564595D

SECONDARY NO CAPACION:
APPLICANT: Gilbert, Teresa

APPLICANT: Gilbert, Teresa

APPLICANT: Gilbert, Teresa

APPLICANT: Gilbert, Teresa

APPLICANT: APPLICANT: SHOUTH FACTOR HOMOLOG ZVEGF4

FILE REFRENCE: 99-19

CURRENT APPLICATION NUMBER: US/09/564,595D

CURRENT FILING DATE: 2000-05-03

PRIOR APPLICATION NUMBER: US 09/304,216

PRIOR FILING DATE: 1999-05-03
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1494 AITITCAICTGAACCCGGAITCTGCAICCACTACAGTAITAICAIGCCACAAGICAGG 1553
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                                                                                                                                                                                                                                                                                                                                  Length 3571;
                                                                                                                                                                                                                                                                                                                             Query Match
45.5%; Score 959.4; DB 4;
Best Local Similarity 70.3%; Pred. No. 6.4e-235;
Matches 1446; Conservative 1; Mismatches 578;
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-111-10
PRIOR PPLIOR TOWN NUMBER: US 60/180,169
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FASTEEQ for Windows Version 4.0
SEQ ID NO 34
                                                                                                                                                                                                                                           ) NAME/KEY: CDS
; LOCATION: (1049)...(2086)
US-09-564-595D-34
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                                                                                                1854 TATTCTGGCCAGGTTGTCTCCTGGTCAAGCGCTGTGGAGGAAATTGTGCCTGTTGTCCC 1913
                                                                                                                                                                                                                        1022 TGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGGATAGCCGCATC 1081
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1794 GCTGCACACCCCGGAACTTCTCAGTGTCCATACGGGAAGAGCTAAAGAGACAGATACCA 1853
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Best Local Similarity 70.3%; Pred. No. 6.4e-235;
Matches 1446; Conservative 1; Mismatches 578; Indels 31; Gaps
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FILE REFERENCE: 98-60C1
CURRENT APPLICATION NUMBER: US/09/706,968
CURRENT FILING DATE: 2000-11-06
PRIOR FILING DATE: 2000-33.31
PRIOR FILING DATE: 2000-33.31
PRIOR FILING DATE: 2000-33.31
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PRIOR FILING DATE: US/09/541,752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2036 CCTGCATTTTAAAAA 2051
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; LOCATION: (1049)...(2086)
US-09-706-968-42
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                                                                                                                                                                                                                                                                                                               542 AAGCTGTGAGTCCTTCAGTGCTACCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATG 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGATGGC 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            662 AGTIGGACTIAGAAGAICIATATAGGCCAACTIGGCAACTICITGGCAAGGCTITIGITT 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       722 TIGGAAGAAAAICCAGAGIGGIGGAICIGAACCIICIAACAGAGGAGGIAAGAIIAIACA 781
                                                                                                                                                                                        482 ATTITICCTICTGAACCAGGGTICTGCATCCACTACAACATTGICATGCCACAATTCACAG 541
                                                             422 TACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAAT 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1854 TATTCTGGCCAGGTTGTCTCCTGGTCAAGCGCTGTGGAGGAAATTGTGCCTGTTGTCCC
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2971 GTTGCTCT-GACAAAAACATATGTATTT-CTTCCTTGTATGGTGCTAGAGCTTAGCGTCA 3028
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                                                                                            1562 AGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAATTAA 1621
                                                                                                                                           2559 GATGCTCTGTTTTCTACAACTCAAAGCTTTTAGAGAGCAGCTATGTTAATAGGAATTAA 2618
                                                                                                                                                                                           1622 ACTIGIGICRIGCIGATAGGACAGACTGGATITITICATATITICATATAAATITICTGCC 1681
                                                                                                                                                                                                                                       2619 A--rereccarecreaaáddaaádacreaacrirircaa-recrireccaacrircceca 2674
                                                                                                                                                                                                                                                                                           1682 ATTTAGAAGAAGAACTACATTCATGGTTTGGAAGAGATAAACCTGAAAAGAAGAGGTGG 1741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1920 -ATTITICIAAACACAATIGITATAGCCAGAGGAACAAGATG---GATATAAAATATT 1975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1976 GTTGCCCTGGACAAAATACATGTATNTCCATCCCGGAATGGTGCTAGAGTTGGATTAAA 2035
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1502 AAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTGCTCATATTCACATATGTAAACC 1561
                                                                                                                                                                                                                                                                                                                          2675 ATTIGGAGGAAAGG---TGCGGTCATGGTTTGGAGAAGCACACCTGCACCAGAGGAGTGG
                                                                                                                                                                                                                                                                                                                                                                                          1742 CCTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTATATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 42, Application US/09457066

Patent No. 6432673
GENERAL INFORMATION:
APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilberson, Debra G.
FILE REFERENCES: 98-60
CURRENT FALLON NUMBER: US/09/457,066
CURRENT FILEO DATE: 1999-12-07
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SOFTWARE: FastSEQ for Windows Version 3.0
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; LOCATION: (1049)...(2086)
US-09-457-066-42
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ORGANISM: Mus musculus
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Db 2973 GTTGCTCT-GACAAAACATATTTTTTATAAAAA 2051  Qy 2036 CCTGCATTTTAAAAAA 2051  Db 3031 TCTGCATTTGAAAAG 3046  RESULT 11 US-09-457-066-6 ; Sequence 6, Application US/09457066 ; Patent No. 6432673 ; GENERAL INFORMATION:		686868
1920 2913 1976	842 ITTICTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGGAACTGTGCCTGTTGTCTCC 901  1854 TATTCTGGCCAGGTTGTCTCCTGGTCAAGGCTGTGGAAAATTGTGCCTGTTGTCTCC 1913  902 ACATTGCAATGAATGTCAATGTGCCCAAGCAAAGTTACTAAAAAAATGCCACGAGGTC 961	6 B 6
1862	1734 ATGGGAAAAAGCAAAGTGGTGAATCTGAATCTCCTCAAGGAAGAGGTAAAACTCTACA 1793 782 GCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCA 841	8 6 8
1802	CAGCCTCTACAAGCCAACATGGCAGCTTTTGGGCAGGCTTTCCTGT CAGGGGGGGGGG	요 중 원
Dy 1742 CCTTATCTTCACTTTATCGATAAGTCAC	AGATCTATATAGGCCAACTTGGCAACTTTTGGCAAGGCAATTTTGGCAACTTTTGGCAAGGCAAGGCTTTTTGGCAAGGCAAGGCAAGGCTTTTTGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	3 & 2
Oy 1682 ATTTAGAAGAAGAACTACATCATGG		ර සි
QY 1622 ACTTGTGTCRTGCTGATAGGACAGACTC Db 2621 ATGTGCCATGCTGAAAGGAAAGACTC	TTCAGTGCTACCCCTTCAGCTTTGCCACTGGACTGCTTAATAATG	ζλ Dp
Oy 1562 AGAACATTCTATGTACTACAAACCTGGT  Db 2561 GATGCTCTGTTTCTACAAACTCAAAGC	482 ATTTTCCTTCTGAACCAGGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCACAG 541	\$ Q
1502	422 TACCAGGAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAAT 481 	දු අ
1442	TAGAAGTTGAGGAGCCCAGTGATGGAAGTTATTAGGGCGCTGGTGGGTTGGTT	3 6 8
Oy 1382 GTTCTGTATTTCAGTTCTTTCGATACGC	CGTTTGATGAAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATTTTG [	8 6
1322	242 GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGGGAAAATGTATGGATACAACTTA 301 	දු පු
1262	TTATTACTGIGIC 	& g
Oy 1202 TTACAGTGCATTCTGAAAGAGGAGACAI	AATTCCAGTTTTCCAGCAACAACAACAAACAAACAAAACAAAACAAAAACAAAAACAAAA	ර සි
Qy 1142 ATGCGTTATCTCCATCCTTAATCTCAGT	GGCGGCCAGAGAGGGGGGGGGGGGGGGGGGGGGGGGGG	3 8 8
	2 CCCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCTAATGAGCCTCTTCGGGCTTCTCCTGG 61	රු ස්

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SCTTTTAGAGAGCAGCTATGTTAATAGGAATTAA 2620
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                                                                                     3ecri----crcaecrecrearecreacrarear 2203
                                                                                                                        ATCAAACAGAATTAGGAGTTGTGCAACAGCTCTT 1261
                                                                                                                                                         rrcrcagrrgrrrgcrrcaaradccrrcccrgc 2263
                                                                                                                                                                                          AAAAGGTCTTCAATCGTGGAAAGAAAATTAAATG 1321
                                                                                                                                                                                                                              ITCAGAGTTACCATGTACGTATTCCACTAGCTGG 1381
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817 GAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGT 876
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          697 CAACTICITGGCAAGGCTTTTGTTTTGGAAGAAAAICCAGAGTGGTGGAICTGAACCTT 756
                                   757 CTAACAGAGGAAGGTAAGATTATACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGG 816
                                                                                                                                   937 GITACTAAAAAAACCACGAGGICCITCAGIIGAGACCAAAGACCGGIGICAGGGGATIG 996
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NAME/KRY: misc_feature
LOCATION: (1015)
OTHER INFORMATION: n = A,T,C or G
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APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Puddington, Christopher S.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Glibertaen West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REFERENCE: 90-001
CURRENT FILING DATE: 2000-11-06
PRIOR PLILING DATE: 2000-11-06
PRIOR PLILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 650 D NOS: 50
LENGTH: 1035
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34.8%; Score 734.4; DB 4;
Best Local Similarity 56.6%; Pred. No. 8.9e-178;
Matches 585; Conservative 261; Mismatches 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 6, Application US/09706968; Patent No. 6528050; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S41 YINCCNYINGAYYINYINAAYAAYGCNATHACNGCNITYWSNACNYINGARGAYYINAIH 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   517 AACAITGICAIGCCACAATICACAGAAGCIGIGAGICCIICAGIGCIACCCCCTICAGCI 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              637 CGATATCTTGAACCAGAGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGG 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CARGCNGARWSNAAYYTNWSNWSNAARTTYCARTTYWSNWSNAAYAARGARCARAAYGGN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 CCNMGNTTYCCNCAYACNTAYCCNMGNAAYACNGTNYTNGTNTGGMGNYTNGTNGCNGTN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 CAGGCGGAATCCAACCTGAGTAGTAATTCCAGTTTTCCAGCAACAAGAACAGAACGGA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 GTACAAGATCCTCAGCATGAGAATTATTACTGTGTCTACTAATGGAAGTATTCACAGC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 CCAAGGITICCICATACTIATCCAAGAAAIACGGICTIGGIAIGGAGATIAGIAGCAGIA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      277 GAGGAAATGTATGGATACAACTTACGTTTGATGAAAGATTTGGGCTTGAAGACCCAGAA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 337 GATGACATATGCAAGTATGATTTTGTAGAAGTTGAGGAACCCAGTGATGGAACTATATTA 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGWSNYTNTTYGGNYTNYTNYTNYTNATNACNWSNGCNYTNGCNGGNCARMGNCARGGNACN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: degenerate sequence derived from SEQ ID NOS: 1 and OTHER INFORMATION: 2
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34.8%; Score 734.4; DB 4; Length 1035;
Best Local Similarity 56.6%; Pred. No. 8.9e-178;
Matches 585; Conservative 261; Mismatches 188; Indels 0;
                                                                                     APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOWOLOG ZVEGF?
FILE REFERENCE: 98-60
CURRENT APPLICATION WUMBER: US/09/457,066
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEG ID NOS: 50
SOFTWARE: FastSEG for Windows Version 3.0
APPLICANT: Gao, Zeren
APPLICANT: Harr, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) NAME/KEY: misc_feature

) LCCATION: (1)...(1035)

; OTHER INFORMATION: n = A,T,C or G

US-09-457-066-6
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                                            CCAAGGITICCICATACTIATCCAAGAAATACGGICTTGGTATGGAGATTAGTAGCAGTA 276
                                                                                      277 GAGGAAAATGTATGGATACAACTTACGTTTGAAGATTTGGGCTTGAAGACCCCAGAA 336
                                                                                                                                    GATGACATATGCAAGTATGATTTTTGTAGAAGTTGAGGAACCCAGTGATGGAACTATATTA 396
                                                                                                                                                                               GGGCGCTGGTGGTTCTGGTACTGTACCAGGAAAACAGATTTCTAAAGGAAATCAAATT 456
157 GTACAAGATCCTCAGCATGAGAATTATTACTGTGTCTACTAATGGAAGTATTCACAGC 216
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Sequence 6, Application US/09564595D
Patent No. 649566B
GENERAL INFORMATION:
APPLICANT: Gilbert, Teresa
APPLICANT: Hart, Charles E.
RESULT 13
US-09-564-595D-6
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118 AGTAAATTCCAGTTTTCCAGCAACAAGAACAGAACGGAGTACAAGATCCTCAGCATGAG 177
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Best Local Similarity 34.5%; Pred. No. 8.2e-36;
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT FILING DATE: 2000-05-03
FRIOR APPLICATION NUMBER: US 09/304,216
FRIOR APPLICATION NUMBER: US 06/164,463
FRIOR PILING DATE: 1999-01-10
FRIOR PLING DATE: 1999-11-10
FRIOR PELICATION NUMBER: US 60/180,169
FRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.0
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LOCATION: (1). .. (1110)
OTHER INFORMATION: n = A,T,C or G
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	0y         772 AGATTATACACCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGAAACTAAAGAA           0p         894 AAGGGTTACACTTCCCGGAATCACTCTGTAACGCTCAGGAAGAACTGTGT           0y         832 ACCATTCTCGCCAGGTTCCTCTGGTAACGCTGTGGTGGTGGTGGTGCTGGTGCT           0y         895 ACCATTCTCCCGCAGGTTCCTCTGGTTGGTGGTGGTGGTGGTGGTGGTGGTGGT	RESULT 15 US-09-564-55D-52   GGUERGE 52, Application US/09564595D   Patent No. 649568   APPLICANT: GABLEAT: Peresa     APPLICANT: GABLEAT: Peresa     APPLICANT: GABLEACH Paul O.     TILLE OF INVENTION: GROWIT FACTOR HOMOLOG ZVEGF4     FILE REPRENCE: 99-19     CURRENT APPLICATION NUMBER: US/09/564,595D     CURRENT FILING DATE: 2000-05-03     PRIOR APPLICATION NUMBER: US 60/164,463     PRIOR FILING DATE: 1999-0-03     PRIOR FILING DATE: 1999-0-04     PRIOR FILING DATE: 1999-0-04     WINDER OF SEQ ID NOWER: US 60/180,169     NUMBER OF SEQ ID NOS: 57     SOFTWARE: ReastSEQ for Windows Version 4.0     TYPE: DNA     CRGANISM: MUS musculus
	REBULT 14 US-09-540-224-3 IS-deterice 3, Application US/09540224 Sequence 3, Application US/09540224 Sequence 3, Application US/09540224 GENERAL INFORMATION: IS-deterice 3, APPLICANT: GIDEN GENERAL INFORMATION: ITLE OF INVENTION: MITTHOOS FOR PROMOTING GROWTH OF BONE, ITLE OF INVENTION: MITTHOOS FOR PROMOTING GROWTH OF BONE, ITLE OF INVENTION: USCAPPABRE: US/09/540,224 CURRENT FILING DATE: 2000-03-31 BARLIER APPLICATION NUMBER: US 60/180,169 SCOFWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 3 LENGTH: 1472 ITYPE: DNA ORGANISM: Mus musculus FEATURE: DNA ORGANISM: Mus musculus FEATURE: US OF WAREVER: CDS US-09-540-224-3	Best Local Similarity

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CACGAGGICCTICAGITGAGACC-----AAAGACCGGIGTCAGGGGATIGCACAAA 1002
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                                                                                                 Query Match
5.6%; Score 117.8; DB 4; Length 1472;
Best Local Similarity 50.9%; Pred. No. 1.6e-20;
Matches 494; Conservative 0; Mismatches 402; Indels 75; Gaps
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; LOCATION: (93)...(1205)
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Search completed: November 26, 2003, 05:52:12 Job time : 116.97 secs 1063 ACAGGAGGATA 1073 1194 CCACCTCGATA 1204 DP ò

Searched:

Run on:

Database

Sequence Sequence Sequence Sequence

DNA CODING

Result No.

sequence seq

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US-UY-852-209A-2

| Sequence 2, Application US/09852209A
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| Patent No. US-2020164687A1
| GENERAL INPORMATION:
| APPLICANT: ERIKSSON, U1f
| APPLICANT: ABE, Kurin
| APPLICANT: DONTEN, Annica
| APPLICANT: DONTEN, Annica
| APPLICANT: DONTEN, Annica
| APPLICANT: DONTEN, Arnica
| TILLE OF INVENTION NUMBER: 60/110, 749
| PRIOR PRILING DATE: 1998-12-18
| PRIOR PRILING DATE: 1998-12-18
| PRIOR PRILING DATE: 1999-07-15
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US-10-143-031A-487
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OTHER INFORMATION: can be a, c, g
     TYPE: DNA
ORGANISM: Homo sapiens
   NAME/KEY: unsure
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0 , Gapext 1.0
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QY         1981         CCTGGACAAAAATACATGTATNTCCATCCCGGAATGGTGCTAGAGTTGGATTAAACCTGC         2040           Db         1981         CCTGGACAAAAATACATGTATNTCCATCCCGGAATGGTGCTAGAGTTGGATTAAACCTGC         2040           QY         2041         ATTTTAAAAAACCTGAATTGGGAANGGAANTTGGTAACGTTGGCCAAANCTTTTTTGAAA         2100           Db         2041         ATTTTAAAAAACCTGAATTGGGAANGGAANTTGGTAAGGTTGGCCAAANCTTTTTTGAAA         2100           QY         2101         ATAATTAAA         2108           Db         2101         ATAAATTAA         2108	RESULT 2 US-10-131-600-2 ; Sequence 2, Application US/10131600 ; Publication No. US/20030082670A1 ; GENERAL INFORMATION:	APPLICANT: ERIKSSON, Ulf APPLICANT: AASE, Karin APPLICANT: LEE, Xuri APPLICANT: PONTEN, Annica APPLICANT: UUTELA, Marko APPLICANT: ALITALO, Kari APPLICANT: ALITALO, Area APPLICANT: ALITALO, Area	APPLICANT: BETSHOLTZ, Christer; 17TLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING 17TLLE OF INVENTION: THEREFOR, AND USES THEREOF; 17TLE OF INVENTION: THEREFOR, AND USES THEREOF; 17TLE OF INVENTION: THEREFOR, AND USES THEREOF; 17TLE OF INVENTION OF THE TREATH OF THE TREATH OF THE TREATH APPLICATION NUMBER: US/10/131,600	CUKKENI FILING DATE: 100-04-05   PRIOR PELING DATE: 1999-09-30   PRIOR PILING DATE: 1999-09-30   PRIOR PILING DATE: 1999-109-109   PRIOR APPLICATION NUMBER: 60/110,749   PRIOR APPLICATION NUMBER: 60/110,749   PRIOR PILING DATE: 1998-11-03   PRIOR APPLICATION NUMBER: 60/113,002	PRIOR FILING DATE: 1998-12-18	ENGTH: YPE: DN RGANISN EATURE: AME/KEY OCATION THER IN	NAME/KEY: unsure  LOCATION: (2065)  COTHER INFORMATION: can be a, c, g or t  FRATURE:  NAME/KEY: unsure  LOCATION: (2070)  COTHER INFORMATION: can be a, c, g or t	) FEATURE: NAME/TEXT: unsure COCATION: (2089) COTHER INFORMATION: can be a, c, g or t US-10-131-600-2	Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 2108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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TGACATCTGCCCTGGCCGGCCAGAGACGAGGACTCAGGCGGAATCCAACCTGAGTAGTA
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             Sequence 1, Application US/10178442
Publication No. US20030113870A1
GENERAL INFORMATION:
APPLICANT: Ferrara, Napoleone
APPLICANT: Kuo, Sophia S.
ITLE OF INVENTION: POLYEPPTIDES HOMOLOGOUS TO FILE REFERENCE: 11659.112USD2
CURRENT APPLICATION NUMBER: US/10/178,442
CURRENT FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: US 09/265,686
PRIOR APPLICATION NUMBER: US 09/265,686
PRIOR APPLICATION NUMBER: US 09/265,686
PRIOR PILING DATE: 1998-11-02
PRIOR FILING DATE: 1998-03-17
NUMBER OS SEQ ID NOS: 8
SOFTWARE: PATENTIN NOWER: US 09/040,220
NUMBER: OS SEQ ID NOS: 8
SOFTWARE: PATENTIN NOS: 8
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Best Local Similarity 97.7%; Pred. No. 0;
Matches 2059; Conservative 1; Mismatches
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LOCATION: (2689)..(2689)
OTHER INFORMATION: Any nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                               TTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAAATTAAAAT
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REPLING DATE: 1998-03-30
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R APPLICATION NUMBER: 60/077641

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R APPLICATION NUMBER: 60/07791

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R APPLICATION NUMBER: 60/078004

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R APPLICATION NUMBER: 60/07886

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ATTTAGAAGAAGAACTACATTCATGGTTTGGAAGAGATAAACCTGAAAAGAAGAGTGG 1741
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                                           1933 ATTTAGAAGAAGAACTACATTCATGGTTTGGAAGAGATAAACCTGAAAAGAAGAGTGG
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CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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Goddard, Audrey
Goddowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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. Sequence 487, Application US/09978295A
; Patent No. US/0020156006A1
; GENERAL INFORMATION:
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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Williams, P. Mickey
Wood, William I.
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Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
Gao, Wel-Qiang
Gerber, Hanspeter
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Desnoyers, Luc
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APPLICANT: Baker Kevin P.
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PRIOR FLING DATE: 1998-05-15
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PRIOR APPLICATION NUMBER: 60/08569
PRIOR FILING DATE: 1998-05-15
PRIOR PLING DATE: 1998-05-15 Query Match 93.9%; Best Local Similarity 97.7%; Matches 2059; Conservative 362 422 62 182 242 490 610 482 542 662 722 250 302 602 850 910 970 셤 à 엄 g 8 6 g ò g ò g ò g 8 셤 Š g ò ద ò ઠે 셤 à ð õ

PRIOR APPLICATION NUMBER: 60/07791
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APPLICATION NUMBER: 60/081203
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APPLICATION NUMBER: 60/081229
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FILING DATE: 1998-04-15
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APPLICATION NUMBER: 60/081819
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APPLICATION NUMBER: 60/080327
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APPLICATION NUMBER: 60/081071
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APPLICATION NUMBER: 60/082700
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                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1998-03-3
      APPLICANT: Wood, ALILIAM 1.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPERENCE: P260PLG9

CURRENT APPLICATION NUMBER: US/09/978,192A

CURRENT FILING DATE: 2001-10-15

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PRIOR PILING DATE: 2001-07-30

PRIOR PILING DATE: 1997-10-17

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PRIOR FILING DATE: 1997-11-3

PRIOR FILING DATE: 1997-11-3

PRIOR PILING DATE: 1998-03-10

PRIOR PILING DATE: 1998-03-11

PRIOR PILING DATE: 1998-03-12

PRIOR PILING DATE: 1998-03-12
        2285 TTTTAAAAAACTGAATT---GGAATAGAATTGGTAAGTT---GCAAAGACTTTTTGAAAA 2338
                                                                                                                                                                             Sequence 487, Application US/09978192A
Patent No. US20020177553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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APPLICATION NUMBER: 60/078910
PILING DATE: 1998-03-20
APPLICATION NUMBER: 60/078939
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Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William I.
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Goddard, Audrey
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Ferrara, Napoleon
Filvaroff, Ellen
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Kuo, Sophia S.
Napier, Mary A.
Pan, James;
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Gao, Wei-Qiang
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PRIOR APPLICATION NUMBER: 60/083322 PRIOR PLILOW DATE: 1980-4-28 PRIOR PLILOW DATE: 1980-4-28 PRIOR PLILOW DATE: 1980-4-28 PRIOR PLILOW DATE: 1980-4-29 PRIOR PLILOW DATE: 1990-4-29 PRIOR PLILOW DATE: 1990-6-3-60 PRIOR PRILOW DAT	PRIOR APPLICATION WUMBER: 60/085704

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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
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Gerritsen, Mary E.
Baker Kevin P.
Botstein, David
Desnoyers, Luc
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Gao, Wei-Qiang
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   1390 ATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGAT 1449
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                                       TTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTT
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Sequence 487, Application US/09999832A Publication No. US20020192706A1 GENERAL INFORMATION: APPLICANT: Ashkenazi, Avi

RESULT 8 US-09-999-832A-487

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PRIOR APPLICATION NUMBER: 60/07920
PRIOR FILING DATE: 1998-03-07
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PRIOR PILING DATE: 1998-04-01
PRIOR PILING DATE: 1998-04-09
PRIOR PILING DATE: 1998-04-05
PRIOR PILING DATE:
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250 CCCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTGC 309 THATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCAA 489 GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACTTA 301 AATTCCAGTTTTCCAGCAACAAGAACAGAACGGAGTACAAGATCCTCAGCATGAGAAA CCCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTGG 62 TGACATCTGCCCTGGCCGGCCAGAGACGAGGGACTCAGGCGGAATCCAACCTGAGTAGTA TTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCAA Gaps Length 2849; 11, 36; Indels DB 10; 93.9%; Score 1979.4; 97.7%; Pred. No. 0; iive 1; Mismatches PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/08359
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PRIOR APLICATION NUMBER: 60/08342
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PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/08032
PRIOR PLING DATE: 1998-04-01
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PRIOR PLING DATE: 1998-04-01
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PRIOR PLING DATE: 1998-04-29
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APPLICATION NUMBER: 60/084366
FILING DATE: 1998-05-05
APPLICATION NUMBER: 60/084414
FILING DATE: 1998-05-06
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CURRENT PILLS UPES 1001-10-15

CURRENT FILING DATE: 2001-10-15

PRIOR PELLOATION NUMBER: 09/09250

PRIOR PELLOATION NUMBER: 00/06250

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PRIOR PELLING DATE: 1997-10-17

PRIOR PELLOATION NUMBER: 60/06250

PRIOR PELLING DATE: 1997-11-21

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PRIOR PELLING DATE: 1998-03-10

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APPLICATION NUMBER: 60/080165
FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080194
                                                                                                                                                                           Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                 Williams, P. Mickey Wood, William I.
      Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
                                                                                                                               Napier, Mary A.
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PRIOR APPLICATION NUMBER: 60/08441  PRIOR PILING DATE: 1998-05-06  PRIOR PILING DATE: 1998-05-07  PRIOR APPLICATION WIMBER: 60/08463  PRIOR APPLICATION WIMBER: 60/084640  PRIOR APPLICATION WIMBER: 60/084640  PRIOR APPLICATION WIMBER: 60/084589  PRIOR APPLICATION WIMBER: 60/084640  PRIOR PLING DATE: 1998-05-07  PRIOR PLING DATE: 1998-05-13  PRIOR APPLICATION WIMBER: 60/085328  PRIOR PLING DATE: 1998-05-15  PRIOR APPLICATION WIMBER: 60/085529  PRIOR PLING DATE: 1998-05-15  PRIOR APPLICATION WIMBER: 60/085580  PRIOR PLING DATE: 1998-05-15  PRIOR PLING DATE: 1998-05-15	Query Match

AAATCACTCACCGACGTGGCCC 1021 IGGCTGATTCTATTAGAGAACGT 1141 AGAACTAAAGAGAACCGATACCA 841 ACTAAAAATACCACGAGGTCC 961 ABGCACAGGAGATAGCCGCATC 1081 AAGGACCTTTCATCTTCAGGAT 1201 TTAGGAGTTGTGCAACAGCTCTT 1261 AATCGTGGAAAGAAATTAAATG 1321 TABAGCTCCATGTCCTGGGCCT 1501 ATGTACGTATTCCACTAGCTGG 1381 TGTCAGTACAGGAAAAAACTG 1441 GCCATATTCACATATGTAAACC 1561 CATTGICATGCCACAATTCACAG 541 SCACTGGACCTGCTTAATAATG 601 CTTCTTGGCAAGGCTTTTGTTT 721 TATCTTGAACCAGAGAGATGGC 661

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970 TTGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACA 1029
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630PIC2: CURRENT APPLICATION NUMBER: US/09/978,608A CURRENT APPLICATION NUMBER: US/09/978,608A CURRENT FILING DATE: 2001-10-16 Prior Application removed - See File Wrapper or Palm SEQ ID NO 487
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97.7%; Pred. No. v,
1, Mismatches
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LOCATION: 2715
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                            ACTIGIGICRIGCIGALAGGACAGACTGGATTITICATATTICTTAAAATTICTGCC
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         <u>AGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAATTAA</u>
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Publication No. US20030045462A1
GENERAL INFORMATION:
APPLICANT: Bakenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Bettein, David
APPLICANT: Eaton, Dan
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Williams, P. Mickey
Wood, William I.
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Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Gerritsen, Mary E.
Goddard, Audrey
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Roy, Margaret Ann
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Kuo, Sophia S.
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Pan, James:
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PRIOR FILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: 60/07968

PRIOR APPLICATION NUMBER: 60/07978

PRIOR APPLICATION NUMBER: 60/07978

PRIOR PILING DATE: 1998-03-27

PRIOR PILING DATE: 1998-03-27

PRIOR PILING DATE: 1998-03-27

PRIOR PILING DATE: 1998-03-37

PRIOR APPLICATION NUMBER: 60/09923

PRIOR APPLICATION NUMBER: 60/09015

PRIOR APPLICATION NUMBER: 60/08015

PRIOR PILING DATE: 1998-03-31

PRIOR PILING DATE: 1998-04-01

PRIOR PILING DATE: 1998-04-05

PRIOR PILING DATE: 1998-04-15

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PRIOR PILING DATE: 1998-04-25

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APPLICANT: Wood, William, P. Mickey
APPLICANT: Wood, William, P. Mickey
TITLE OF INVENTION: Acids Encoding the Same
FILE REPRENCE: P2330PLG4
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US/09/978,191A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/91885
PRIOR PLILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06250
PRIOR PLILING DATE: 1997-11-13
PRIOR PLILING DATE: 1997-11-13
PRIOR PLILING DATE: 1997-11-21
PRIOR PLILING DATE: 1997-10-17
PRIOR PLILING DATE: 1998-03-11
PRIOR PLILING DATE: 1998-03-12
PRIOR PLILING DATE: 1998-03-13
PRIOR PLILING DATE: 1998-03-25
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PRIOR PLING DATE: 1998-03-25
PRIOR PLILING DATE: 1998-03-25
PRIOR PLING DATE: 1998-03-25
PRIOR PLING DATE: 1998-03-25
                                Sequence 487, Application US/09978191A
Publication No. US20030050239A1
GENERAL INPORMATION:
APPLICANT: Baker Kevin P
APPLICANT: Beker Kevin P
APPLICANT: Bettein, David
APPLICANT: Bettein, David
APPLICANT: Eaton, Dan
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kluo, Sophia S.
Napier, Mary A.
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PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
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Williams, P. Mickey
Wood, William I.
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Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
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Paoni, Nicholas F
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APPLICANT:
APPLICANT:
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TATTACTGCTCTCGAAGGATTCCCAAGGCTTCCCCAAGGTTTCCCAAGGTTTCCCAAGGTTTCCCAAGGTTTTCCCAAGGTTTTCCCAAGGTTTTCCCAAGGTTTTCCCAAGGTTTTCCCAAGGTTTTCCCAAGGTTTTCCCAAGGTTTTCCCAAGGTTTTCCCAAGGTTTTCCCAAGGTTTTCCCAAGGTTTTCCCAAGGTTTTCCCAAGGTTTTCCCAAGGTTTTCCCAAGGTTTTCCAAGAAAAAAAA	TAGTACCECTTCAACCTTTGACATTAAAAAAAA	1150   ACAATTGCAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAATACCACGAGGTCC   1150   ACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAATACCACGAGGTCC   1209   962   TTCAGTTGAGACCAAAGCTCACGACGTGCCC   1209   1210   TTCAGTTGAGACCAAAGCTCACGACGAGGTCC   1269   1210   TTCAGTTGAGACCAGAGCAGTGCAGAGAATTGCACAAATCACTCAC
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RIOR APPLICATION NUMBER: 60/083499  RIOR APPLICATION NUMBER: 60/083545  RIOR FILING DATE: 1998-04-29  RIOR FILING DATE: 1998-04-29  RIOR FILING DATE: 1998-04-29  RIOR FILING DATE: 1998-04-29  RIOR PLING DATE: 1998-04-29  RIOR APPLICATION NUMBER: 60/08359  RIOR PLING DATE: 1998-04-29  RIOR APPLICATION NUMBER: 60/08350  RIOR PLING DATE: 1998-04-29  RIOR APPLICATION NUMBER: 60/083742  RIOR PLING DATE: 1998-04-30  RIOR PLING DATE: 1998-04-30  RIOR PLING DATE: 1998-04-30  RIOR PLING DATE: 1998-04-30  RIOR APPLICATION NUMBER: 60/084366  RIOR PLING DATE: 1998-05-06  RIOR PLING DATE: 1998-05-07  RIOR RELING DATE: 1998-05-07  RIOR PLING DATE: 1998-05-07  RIOR RELING DATE: 1998-05-07  RIOR PLING DATE: 1998-05-07  RIOR RELING DATE: 1998-05-07  RIOR PLING DATE: 1998-05-07		

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APPLICANT: GOTHER H, ANGELT, MISSELL APPLICANT: MISSELL APPLICANT: NO. 60phia S. APPLICANT: Thurst. District Control of the C
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
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                                                                                            1690 TGCAAGTGACCCTGATTCCGTTGCCTTGCTTAACTCTAAAGCTCCATGTCCTGGGCCT 1749
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      GITCIGIAITICAGIICITICGAIACGGCITAGGGIAAIGICAGIACAGGAAAAAAACIG 1441
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                                                             TIGIATIAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGG
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Publication No US20030050240A1
GENERAL INFORMATION:
APPLICANT: Baker Kevin P.
APPLICANT: Bockstein, David
APPLICANT: Bockstein, David
APPLICANT: Beronyers, Luc
APPLICANT: Ferrara, Napoleon
APPLICANT: Ferrara, Napoleon
APPLICANT: Forony, Sherman
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
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PRIOR APPLICATION NUMBER: 60/080107
PRIOR PILING DATE: 1998-03-31
PRIOR PILING DATE: 1998-04-01
PRIOR PILING DATE: 1998-04-09
PRIOR PILING DATE: 1998-04-05
PRIOR PILING DATE: 1998-04-15
PRIOR PILING DATE: 1998-04-22
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TGACATCTGCCCTGGCCGGCCAGAGACAGGGACTCAGGCGGAATCCAACCTGAGTAGTA 369 250 ccceccerdadreadcrereaceceadreadecaarreadecrerredegerrerecide 309 TGACATCTGCCCTGGCCGGCCAGAGACGAGGGACTCAGGCGGAATCCAACCTGAGTAGTA 121 AATTCCAGTTTTCCAGCAACAAGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGA 181 GAAATACGGICTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACTTA 301 430 TTATTACTGTGTCTACTAATGGAAGTATTCACAGGCCCAAGGTTTCCTCATACTTATCCAA CGTTTGATGAAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATTTTTG TTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCAA CGTTTGATGAAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATTTTG GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACTTA Gaps Length 2849; 11; CCCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCAAATGAGCCTCTTCGGGCTT 36; Indels DB 11; Score 1979.4; Pred. No. 0; 1; Mismatches PRIOR PILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/08436
PRIOR PILING DATE: 1998-05-05
PRIOR PILING DATE: 1998-05-06
PRIOR PILING DATE: 1998-05-06
PRIOR PILING DATE: 1998-05-06
PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-05-07
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PRIOR APPLICATION NUMBER: 60/084639
PRIOR PILING DATE: 1998-05-07
PRIOR PELING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/08539
PRIOR PELING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/08558
PRIOR PELING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/08558
PRIOR PILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08559
PRIOR PILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08559
PRIOR PILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15 Query Match
Best Local Similarity 97.7%;
Matches 2059; Conservative 122 310 370 62 182 490 550 242 302 셤 ð a ò 셤 ð g ò 엄 ò g

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FRIOR FILING DATE: 1998-04-01 FRIOR APPLICATION NUMBER: 60/081070 FRIOR APPLICATION NUMBER: 60/081049 FRIOR FILING DATE: 1998-04-08 FRIOR FILING DATE: 1998-04-08 FRIOR FILING DATE: 1998-04-08 FRIOR PRILATION NUMBER: 60/081071 FRIOR PILING DATE: 1998-04-08	FILING DATE: 1998-04 FILING DATE: 1998-04 APPLICATION NUMBER: FILING DATE: 1998-04	FILING PELLICATION NOMBER: 80/081229 FRIOR FILING DATE: 1998-04-09 FRIOR PILING DATE: 1998-04-09 FRIOR FILING DATE: 1998-04-15 FRIOR FILING DATE: 1998-04-15 FRIOR PILING DATE: 1998-04-17	FILING DATE: 1998-04		; PRIOR APPLICATION NUMBER: 60/082568 ; PRIOR FILING DATE: 1998-04-21 ; PRIOR APPLICATION NUMBER: 60/082569	; PRIOR FILING DATE: 1998-04-21 ; PRIOR APPLICATION NUMBER: 60/082704 ; PRIOR FILING DATE: 1998-04-22 ; PRIOR APPLICATION NUMBER: 60/082804	PRIOR FILING DATE: 1998-04-22 PRIOR APPLICATION NUMBER: 60/082700 PRIOR FILING DATE: 1998-04-22	; PRIOR APPLICATION NUMBER: 60/082797 ; PRIOR FILING DATE: 1998-04-22 ; PRIOR APPLICATION NUMBER: 60/082796	; PRIOR FILING DATE: 1998-04-23 ; PRIOR APPLICATION NUMBER: 60/083336 ; PRIOR FILING DATE: 1998-04-27	FRIOR FILING DATE: 1998-04-28 FRIOR PELLING DATE: 1998-04-28 FRIOR APPLICATION NUMBER: 60/083392		FILDER AFFLICATION NUMBER: 00/083450 FRIOR FILING DATE: 1998-04-29 FRIOR PELICATION NUMBER: 60/083499 FRIOR PILING NAME: 10000	APPLICATION NUMBER: FILING DATE: 1998-04	APPLICATION N FILING DATE: APPLICATION N	; PRIOR FILING DATE: 1998-04-29 ; PRIOR APPLICATION NUMBER: 60/083559 ; Daton ETTING NAME: 4000-04-30	APPLICATION N	APPLICATION NUMBER: FILING DATE: 1998-04	; PRIOR APPLICATION NUMBER: 60/084366 ; PRIOR FILING DATE: 1998-05-05 ; PRIOR APPLICATION NUMBER: 60/084414	FILING DATE: 1998-05 APPLICATION NUMBER:	FILING DATE: 1998-05 APPLICATION NUMBER:		APPLICATION N
t. sy ind Transme	LON: ACIGS E P2630P1C25 FION NUMBER: DATE: 2001-1	R FILING DATE: 2001-0/-30  R PILING DATE: 1997-10-17  R PELING DATE: 1997-10-17  R APPLICATION NUMBER: 60/064249	ATTON NUMBER: 60/065311 DATE: 1997-11-13 ATION NUMBER: 60/066364	DATE: 1997-11-21 ATION NUMBER: 60/077450   DATE: 1998-03-10   DATION NUMBER: 60/077632	DATE: 1998-03-11 ATION NUMBER: 60/077641 DATE: 1998-03-11	ATION NUMBER: 60/07/649 DATE: 1998-03-11 ATION NUMBER: 60/077791 DATE: 1998-03-12	ATION NUMBER: 60/078004 DATE: 1998-03-13 ATION NUMBER: 60/078886	DATE: 1998-03-20   ATION NUMBER: 60/078936   DATE: 1998-03-20	ATION NUMBER: 60/078910  DATE: 1998-03-20  PATION NUMBER: 60/078939	ATION NUMBER: 60/079294 DATE: 1998-03-25 DATE: 1998-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-	ALIUN NUMBER: 00/0/2020 : DATE: 1998-03-26 ALION NUMBER: 60/079664	ATTON NUMBER: 60/079689 ATTON NUMBER: 60/079689 DATE: 1998-030-27	DATE: 1998-03-27 ATION NUMBER: 60/079728	DATE: 1998-03-27	ATION NUMBER: 60/079920 DATION NUMBER: 1998-03-30 ATTON NUMBER: 60/07993	DATE: 1998-03-30 ATION NUMBER: 60/080105	DATE: 1998-03-31 AAIION NUMBER: 60/080107	FILLING DATE: 1998-03-51 APPLICATION NUMBER: 60/080165 FILLING DATE: 1998-03-31	60/ 3-31	ASPELICATION NUMBER: 60/080327 FILING DATE: 1998-04-01 ADPLICATION NUMBER: 60/080328	1998-04-01 NUMBER: 60/	FILING DATE: 1998-04-01 APPLICATION NUMBER: 60/080334

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TIGIATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGG 1381
                                                                                                                                                                                                                                                                                                                                 TTACAGTGCATTCTGAAAGAGGACACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2826)
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Contact: MGC help desk
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Tissue Procurement: CLONTECH
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                                                                           Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 41 Row: g Column: 9
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9994186 This clone has the following problem: frame shifted.
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                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                         Length 2826,
                                                                                                                                                                                                                                                                                                                                                                                                          73;
   http://www-shgc.stanford.edu
(Dickson, Mark) mcd@paxil.stanford.edu
M., Schmutz, J., Grimwood, J., Rodriquez,
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                             DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                          38;
                                                                                                                                                                                                                                                                                                                                                                         Score 1894.2; DB 11
Pred. No. 5.6e-298;
1; Mismatches 38;
                                                                                                                                                                                                                                                                                                                              846
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                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9666"
/clone="ThAMGE:4614150"
/tissue_type="Kidney"
/clone="tip="will midc_75"
/lab_host="bull OB"
/note="vector: pDNR-LIB"
a 519 c 591 g 846
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 94.8%;
Matches 2057; Conservative
                   Contact:
Dickson, PR. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 729
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement. ATC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Library Preparation: Life Technologies, Stanford Human Genome
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web Site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
                                                                                                                                                                          Genome
CA 94305
                                                                                                                                                                                                                                                                                                                                                found
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                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 110 Row: p Column: 4 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9994186 This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --GGAGTACAAGATCCTCAGCATGAGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:6527736"
/tissue type="Uterus, leiomyosarcoma"
/clone lib="NIH MGC 71"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1892.4; DB 1
Pred. No. 1.1e-297;
1; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pCMV-SPORT6"
479 c 551 g 803 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.8%;
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Best Local Similarity 94.8
Matches 2056; Conservative
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ORIGIN
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Schener, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
McKernan, K.J., Mallahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, X.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, F.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schmutz, J., Myere, R.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Sanius, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2039
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                                                                                                                                                                                  CATITITAAAAAACCIGAAITGGGAANGGAANTIGGIAAGGITGGCCAAANCTITITGAA 2099
                                                              GGCCTTATCTTCACCTTTATCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTATA 1799
                                                                                                           GGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTTATA 2048
                                                                                                                                                                                                                                                                                                                                                     ATTITICTAAACACAATIGITATAGCCAGAGGAACAAAGATGGATATAAAAATATIGTTG 1979
               CCATTTAGAAGAAGAACTACATTCATGGTTTGGAAGAGATAAACCTGAAAAGAAGAGT 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 2655)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (01-MAY-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                   CCAAAGGTATTTAATATTCTTTTTATGACAACTTAGATCAACTATTTTTAGGCTTGGTAA
                                                                                                                                                           TTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTTAAATATATCTATTTTA
                                                                                                                                                                                                                                                        CCAAAGGTATTTAATATTCTTTTTATGACAACTTAGATCAACTATTTTTAGCTTGGTAA
                                                                                                                                                                                                                                                                                                                                                                                                  2169 ATTITICIAAACACAATTGTTATAGCCAGAGGAACAAAGATG---ATATAAAATATTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1980 CCCTGGACAAAATACATGTATNTCCATCCCGGAATGGTGCTAGAGTTGGATTAAACCTG
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                                                                                    /tissue type="cecum"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
dev gtage="adult"
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                                                                                                                                                                                                                                                                            /note="unnamed protein product; platelet-derived growth factor, C polypeptide (MGD|MGI:1859631, GB|NM_019971, evidence: BLASTN, 99%, match=2691)
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Functional annotation of a full-length mouse cDNA collection and strong and strong and strong and strong annotation of a full-length mouse cDNA collection and strong and stro
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Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 tull-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3244)
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
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/Brzain="C57BL/63"
/db_xref="FANTOM DB:9130403008"
/db_xref="taxon:10090"
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SIIMPQVTETTSPSVLPPSSLSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKP
TWQLLGKAFLYGKKSKVVNLNLLKEEVKLYSCTPRNFSVSIRBELKRTDTIFWPGCLL
VKRCGGNCACCLHNCNBCQCVPRKYTKKYHEVLQLRFKTGVKGLHKSLTDVALEHHEE
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/protein id="BAC35216.1"
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RHERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDD
                          Quackenbush, J., Schrim, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Boffelli, D., Bolunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fufita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodxiguez, I., Sakamoto, N., Sasaki, H., Stochbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., and Hayashizaki, X., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adachi, J. Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayasahida, K., Hayatsu, N., Hiramcto, K., Hiracka, T., Hirozane, T., Harotani, K., Ishi, Y., Itoh, M., Kagawa, I., Kaukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Korthara, C., Mareuyama, T., Miyazaki, A., Murata, M., Nakhi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saito, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sagabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tanamatsu, M., and Hayashizaki, Y., Tayawi, Y., Tayawi, Y., Tayawi, Y., Tayaki, Y., Tayaki, Y., Tayawi, Y., Tayaki, Y., Tayawi, Y., Tayaki, Y., Y., Tayaki, Y., Y., Y., Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 tull-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2765)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001) 21085660 11217851
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Fax:81-45-503-9216)
                Pesole, G.,
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                   Matsuo, Y., Nikaido, I.,
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/db_xref="FANTOM_DB:D930001M08"
/db_xref="taxon:10090"
/clone="D930001M08"
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itch, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Arakawa, M., Ishahi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Saito, T., Saito, T., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaldo, I., Resole, G., Kochiwa, H., Wagner, L., Washlo, T., Satali, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bolinga, N., Carninci, P., de Bonaldo, M.F., Erownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N. H., Lyons, P., Nordone, P., King, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weltz, C., Whittaker, C., Wilming, L., Massinzaki, Y., Savashiza, Y., Savaita, X., Tasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.
Punctional annotation of a full-length mouse cDNA collection
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                                                                                                                                                                                                                                                                                           AK042767

Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730022G11 product:platelet-derived growth factor, C polypeptide, full insert sequence.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new GGENOME Res. 10 (10), 1617-1630 (2000)
                                                                    2196 GTIGCTCT-GACAAAAACATAIGIAITT-CTTCCTTGTATGGTGCTAGAGCTTAGCGTCA
2136 ITITITICIAAACAAAATIGITATAGCCAGAAGAACAAAGATGATIGATATAAAAATCIT
                                            GTTGCCCTGGACAAAATACATGTATNTCCATCCCGGAATGGTGCTAGAGTTGGATTAAA
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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AK042767.1 GI:26335314
AK042767.1 GI:26335314
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/mol type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM DB:A730022G11"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="A730022G11"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research (RIKEN), Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome-gsc.riken.go.jp, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                               Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 470, 1412-14054 (2002)
( (bases 1 to 3405)
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
1. .3405
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Pred. No. 5.9e-146;
1; Mismatches 579;
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 35 Row: p Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: marched mRNA gi: 10242384
This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 cecececicadarandecerececedarendecanandereceredadeereereereere
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                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2893)
                                                                                                                    Strausberg_R.
Direct Submission
Submission
Submitted (01-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGACATCTGCCCTGGCCGGCCAGAGACGGAGGACTCAGGCGGAATCCAACCTGAGTAGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue type="Mammary tumor metastatized to lung.
MMTV-LTR/Wnt1 model. Expression driven by an MMTV-LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S.M.
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Martin, R.G., Muzny,
                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gibert Smith, Ph.D.
CDNA Library Arrayed by: The I-M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2893;
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Pred. No. 3.7e-135;
1; Mismatches 578; J
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Center code: BCM-HGSC
Center code: BCM-HGSC
Contact: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Huly/
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart.
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="NCI CGAP_Lu30"
/lab host="DH10B"
/note="Vector: pCMV-SPORT6"
597 c 650 g 778 t
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/clone="IMAGE:3660797"
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/strain="CZECH II"
musculus (house mouse)
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Mus musculus, Similar to platelet-derived growth factor, C polypeptide, clone IMAGE:3660797, mRNA.
BC029099
GI:20809397
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  ATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGAT 1201
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                                                   CTTCATCCCCACCAGCGTTGGCCGCAGGGCTC----TCAGCTGCTGATGCTAGGT
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BQ068266 399 bp mRNA linear EST 02-APR-2002 AGENCOURT 6794408 NIH\_MGC\_121 Homo sapiens cDNA clone IMAGE:57705105', mRNA sequence. 1920 2187 2305 1742 1802 2067 1862 2127 TITITICIAAACACAATIGITATAGCCAGAGGAACAAAGATG---GATATAAAATATTGT 1977 1443 GCAAGTGAGCACCTGATTCCGTTGCCTTAACTCTAAAGCTCCATGTCCTGGGCCTA 1502 AAATCGTATAAAATCTGGATTTTTTTTTTTTTTTGCTCATATCACATATGTAAACCA 1562 1779 Arrergaadragaaaracriegariricrecaace---rerirecaradaaragaca 1835 1719 AGTTGİTCTTGİTAİĞGGCAAĞİGATGİCAGCACAAAAAAİTĞGİGAAAAAÇACACAÇTİG 1778 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 (hases 1 to 999)
National intp://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC) Unpublished
Contact: Robert Strausberg, Ph.D. TCCTITTGACATTATAACTGTTGGCTTTTCTAATCTTGTTAAATATATCTATTTTTACCA AAGGTATTTAATATTCTTTTTATGACAACTTAGATCAACTATTTTTAGCTTGGTAA--A AAGGIAFITIAATATICITITITIATGACAACCIAGAGCAATTATTTTAGCITGATAATTT TGCCCTGGACAAAATACATGTATNTCCATCCCGGAATGGTGCTAGAGTTGGATTAAAACC CTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTTATATTC GAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAATTAAA CTTGTGTCRTGCTGATAGGACAGACTGGATTTTTCATATTTCTTATAAAATTTCTGCCA TTTAGAAGAAGAACTACATTCATGGTTTGGAAGAGATAAACCTGAAAAGAAGAGTGGC 1836 AIGCICIGITITCTACAAACTCAAAGCTITIAGAGAGCAGCTAIGTTAATAGGAAITAAA Email: cgapbs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation

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| organism="Homo sapiens"
| mol_type="mRNA"
| db_xref="taxon:9606"
| clone="IMAGE:4750095"
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLANL333 row: k column: 23
High quality sequence stop: 676.
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BG677432 1NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4750095 5',
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/lab host="DH10B (T1 phage-resistant)"
/clone_lib="NOI GAAP SKN4"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NOI_CGAP Library."

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MH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
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                                      661 AAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGTAAGATTATACAGCTGCAC
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Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Flate: LLAMM0604 row: f column: 16
High quality sequence stop: 764.
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Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McBligott, K., Boozer, S., Mays, R., Smith, S., Velseo, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J.J., Danzig, J. and Ducar, M. Creation of genome-wide protein expression libraries using random activation of gene expression.

Nat. Biotechnol. 19 (5), 440-445 (2001)

44115,

Athersys, Inc. 3201 Carnegle Ave, Cleveland, OH 711: 216 431 9900 Fax: 216 361 9596

Contact: Scott J. Cain

21227151

Email: scain@athersys.com High quality sequence stop: 485. Location/Qualifiers

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MEDLINE
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                                          TGTCAATGTGTCCCAAGCAAAGTTACTAAAAATACCACGAGGTCCTTCAGTTGAGACCA 975
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_tref="txxxxn:9606"
/clone_lib="HT1080"
/clone_lib="HT1080"
/clone_sise 'Creation of Genome-wide Protein Expression
Inbrarise using Random Activation of Gene Expression',
Inbrarise using Random Activation of Gene Expression',
Inbrarise using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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97.8%;
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Matches 788; Conservative
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EST 21-APR-2001

mRNA linear EST 21-APR sapiens cDNA, mRNA sequence

RST4916 Athersys RAGE Library Homo BG185961

BG185961.1 GI:13707648 Homo sapiens (human) Homo sapiens

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 9 BG185961 LOCUS

REFERENCE

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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603394005F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5404105 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGC
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                                                                                                                                                       GCTTTAGTTTTTGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTA
                                                                                                                                                                                                                                   AGATTATACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGA
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                                                        GAGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAG
                                                                             GAGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAG
                                                                                                                                                                                                                                                                                  832 ACCGATACCATTITICIGGCCAGGIIGICICCIGGIIAAACGCIGIGGIGGGAACIGIGCC
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                                                                                                                                GCTTTTGTTTTTGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTA
                                                                                                                                                                                                        772 AGATTATACAGCTGCACACCTCGTAACTTCTCAGTGTCCCATAAGGGAAGAACTAAAGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Site_2: Sall; Cloned unidirectionally. Primer: Ollgo dT. Average insert size 1.5kb. Library constructed by Life
Technologies Note: this is a NCI_CGAP Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                      1142 bp mRNA linear EST 01-MAY-2001
602627750F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4752348 5',
mRNA sequence.
                                                                               ACCACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTCAGGGGATTGCACAAATCACTCA 1009
                                                                                                                                                       GATAGCCGCATCACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCAGTGGCTGATTCT 1129
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                                                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMIGOLO row: d column: 13
High quality sequence stop: 803.
                                                                                                                                                                             CAATTCACAGAAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1142)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 759.2; DB 10; Length 1142;
Pred. No. 1.3e-113;
0; Mismatches 28; Indels 3;
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                                                                                                                                                                                                                                                                                                           1130 ATTAGAGAACGTATGCGTTATCTCCA 1155
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Best Local Similarity 96.3%;
Matches 809; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
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AUTHORS
TITLE
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
   Tissue Procurement: Dr. Eliot Spindel
   CDNA Library Preparation: CLONTECH
   CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
   DNA Sequencing by: Agencourt Bioscience Corporation
   Clone distribution: NCI-CGAP clone distribution information can be
   found through the I.M.A.G.E. Consortium/LLNL at:
   http://image.llnl.gov
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   High quality sequence stop: 590.
   High quality sequence stop: 590.
   i. Cottion/Qualifiers
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Average insert size 1.0-4:0 Nb. Tissue pooled from
pre-pubertal, post pubertal sn menopausal monkeys.
Constructed by Clontech, Note: this is a NICHD Library."
                                                                                                                                                                                                                                                                                                                                                                    CB309471 AGENCOURT 11834776 NICHD Rh Ov1 Macaca mulatta cDNA clone IMAGE:6893055 5', mRNA sequence.
                                                         1384 TCTGTATTTCAGTTCTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAAACTGTG 1443
658 GTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGT 717
                                                                                        CITAGAAGAICTATATAGGCCAACTIGGCAACTICTIGGCAAGGCTITIGITTIGGAAG 728
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Macaca mulatta
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence stop: 791.
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0; Mismatches 11;
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/tissue types="Chondrosarcoma"
/dev stage="Adult"
/lab_host="NHIDB (Life Technologies)"
/clone lib="NCI CGAP EDI"
/clone lib="NCI CGAP EDI"
/note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
/pharmacia) with a modified polylinker; Site_1: ECOR I;
/site_2: Not I; NCI CGAP EDI is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line CS5. The library was constructed according to Bonaldo
.Lemnon and Soares, Genome Research, 6:791-806, 1996.
/i.ennon and Soares, Genome Research, 6:791-806, 1996.
/rist strand cDNA synthesis was primed with an oligo-dT
primer containing a Not I site. Double stranded cDNA was
ligated to an ECOR I adaptor, digested with Not I, and
cloned directionally into pT7T7-Pac vector: The
oligonicleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GCTCRAGGCT.
TAG LIB=UI-H-EDI
TAG TISSUE=chondrosarcoma
TAG SESC-CGTAGGCT"
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UI-H-EDI-axw-j-04-0-UI.s1 NCI_CGAP_ED1 Homo sapiens CDNA clone
IMAGE:5834595 3', mRNA sequence.
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                                                                                                                                                                                                                                                     CCATGAGGAGTGTGACTGTGTGCAGAGGAGCACAGGAGGATAGCCGCATCACCACCA 1088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
POLYA-Yes.
                                                                                                                                                                896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           542
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                                                                                GCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACTGTGCCTGTTGTCTCCCACAATTG
                                                                                                                                                                                                            GCAGCTCTTGCCCCAGAGCTGCAGTGCAGTGCTGATTCTATTAGAGAACGTATGCGTT
                                                                                                                                                                CAATGAATGTCAATGTCCCCAAGCAAAGTTACTAAAAATACCACGAGGTCCTTCAGTT
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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BQ015321/c
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1393

328

268

1453

208

1513

28

1273

2

Gaps

2, 686;

Indels

568

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Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Pukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashu, N., Hiranco, K., Hara, A., Hashizume, W., Hayashu, N., Hiranco, K., Hara, T., Hirozane, T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, M., Muzata, M., Makamura, M., Nishi, K., Nomura, K., Nimazaki, R., Ohno, M., Ohasto, N., Sano, H., Sasai, D., Shibata, K., Shinagawa, A., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, T., Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research Group, RIKEN Golences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (R-mail:genome-reseascriken.go.)p, Rangawa, 230-0045, Japan (R-mail:genome-reseascriken.go.)p, Tel:R1-8-503-9222, Pax: 81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/.
URL:http://fantom.gsc.riken.go.jp/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue type="head"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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/strain="C57BL/6J"
/db_xref="FANTUM DB:C130008P20"
/db xref="Faxon:1009"
/db cref="taxon:1009"
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of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 6 (bases 1 to 2502) Adachi,J., Aizawa,K., Akimu
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                                                                                                                                                              Mus musculus 16 days embryo head cDNA, RIKBN full-length enriched library, clone:Cl30008P20 product:platelet-derived growth factor, C polypeptide, full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsunoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yonaca,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
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Analysis of the mouse transcriptome based on functional annotation
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Nature 409 (6821), 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
                                                                                                                                                                                                                                                                                                                                                        AK081347.1 GI:26099857
HTC; CAP trapper.
Mus musculus (house mouse)
      1633 GCTGATAGGACAGA 1646
                                                           27 GCTGATAGGAAAA 14
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1.789
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/note="vector: pCNV-SPORT6; Site_l: NotI; Site_2: BcoRV
/note="pred; primed and information and information and information and information and information and information insert size is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3; kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH MGC Library.
37 a 158 c 186 g 208 t
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Pred. No. 4.8e-89;
0; Mismatches 8; Indels
                 90
http://image.llnl.gov
Plate: LiAM11538 row: k column:
High quality sequence start: 26
High quality sequence stop: 762.
Location/Qualifiers
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90.8%;
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603065222F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5214461 5',
mRNA sequence.
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Catarrhini; Hominidae; Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                  GAAGACCCAGAAGATGACATATGCAAGTATGTTTGTAGAAGTTGAGGAACCCAGTGAT
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
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Mammalia; Eutheria; Primates;
1 (bases 1 to 789)
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TITLE
JOURNAL
COMMENT
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 700 CTTCTTGGCAAGGCTTTTTTTTGGAAGAAAA
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 750 CTTCTTGGCAAGGCTTTTTTTTGGAAGAAAA
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Search completed: November 26, 2003, 05:47:45 Job time : 3097.58 secs Human VEGF-X prote Human VEGF-X prote Human 990126vegx p Human PRO200 (vasc Human PRO200 prote Human PRO713 prote Human TANGO 128. Human TANGO 128. Bone morphogenic p Human zvegf3 polyp Polypeptide for hu Human VEGF/PDGF

Human 1994, a PDGF-Human 2vegf3 prote Human PRO200 prote Human PRO200 prote Human anglogenesis Human vascular end Human VEGF-like pr Human VEGF-like pr

Human zvegf3. Hom Human zvegf3 prote Human growth facto Human PRO polypept Human secreted/tra Novel secreted and Human PRO200 polyp

Human PRO200 polyp Human vascular end Human VEGF-X prote Human VEGF-X prote Human Growth facto Human growth facto Human VEGF-X prote Human VEGF-X prote

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Platelet-derived growth factor C; PDGF-C; cell proliferation; growth factor; heparin; connective tissue; wound healing; VEGF-F; fibroplast mitogenesis; PDGF alpha receptor activation; tumour growth; choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia; lung carcinoma; erythroleukemia; tissue remodelling.
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                                                                                     AAB01419
AAY96858
AAA65603
AAG65603
AAG104465
AAU04465
AAU12314
AAB14028
AAE02649
AAE0997
AAB49895
AAB50980
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AAB47889
AAU76684
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ABU66712
ABU66988
ABU59793
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ABG72132
AAB10639
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AAB10636
AAB03003
AAB10640
AAB10641
                                    AAB10651
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98US-0110749.
98US-0113002.
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12-NOV-1998;
03-DEC-1998;
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Human platelet-der
Human VEGF-E prote
Human PRO200 prote
Human vascular end
Human zvegf3, SEQ
Human platelet-der
Human PRO200 (UNQ)
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                                                                                                                                                           1 MSLFGLLLVTSALAGQRRGT.....DVALEHHEECDCVCRGSTGG
                                                                                                                                                                                                                                                      1107863
        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                          1107863 seqs, 158726573 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                          protein search, using sw model
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AAE13212
AAY3176
AAY30023
AAB48657
AAB48657
AAB444322
AAB10633
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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                                                          protein -
                                                                                                                                                             Sequence:
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Database

10 m 4 m 9 r m b

Result Š. Human

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The present sequence represents human platelet-derived growth factor C (PDGF-C) (formally designated VBGF-F). PDGF-C polypeptides have the ability to stimulate and enhance proliferation or differentiation, and/or growth or motility of cells expressing a PDGF-C receptor.

C and/or growth or motility of cells expressing a PDGF-C receptor.

CC PDGF-C polypeptides can be used in pharmaceuticals for promoting cell proliferation, preferably in combination with one other growth factor and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also be used for stimulating connective tissue or wound healing. The PDGF-C polypeptide can be enzymatically processed to generate the active truncated form of PDGF-C and used to regulate the receptor-binding mitogenesis in a mammal and to induce PDGF and used to promote fibroblast mitogenesis in a mammal and to induce PDGF and processing PDGF-C and used to inhibit tumour growth of a tumour CDGF-C antagonists can be used to inhibit tumour growth of a tumour corricoarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma and erythroleukemia, can be identified by testing for expression of confocalling during invasion of tumour cells into a normal population of cells. Antagonists can also be used to treat fibrotic conditions,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVERESDGTIL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRFPHTYPRNTVLVWRLVAVERVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTIL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSLFGLLLVTSALAGORRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation, differentiation, growth and motility of cells expressing the PDGF-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRWCGSGTVPGKQISKGNQIRIRFVSDBYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA
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                                       Uutela M, Alitalo
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100.0%; Pred. No. 1.4e-179;
ive 0; Mismatches 0;
                                       Ponten A,
(UYHE-) UNIV HELSINKI LICENSING LTD
                                       Lee X, Pont
Betsholz C;
                                                                                                                                                                                                                                     Claim 27; Fig 2; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 345; Conservative
                                       Aase K,
Heldin C,
                                                                                                WPI; 2000-292954/25.
N-PSDB; AAA12523.
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                                 Eriksson U,
                                                        Oestman A,
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LTEBVRLYSCTPRNFSVSIREELKRIDIIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300 VIKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEBCDCVCRGSTGG 345 VTKKYHEVLQLRPKTGVRGLHKSLTDVALBHHEECDCVCRGSTGG 345 241 241 301 301 181 g g ò à

120

9 9 180

240

AAY33679 standard; Protein; 345 AA.

AAE13212 standard; Protein; 345

(first entry)

12-FEB-2002

AAE13212

RESULT 2
AAE13212
ID AAE1
XX
AC AAE1
XX
DT 12-F

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The patent discloses a method for producing a transgenic, non-human animal over-expressing a platelet derived growth factor C (PDGF-C), or its functional fragment or analogue. The method involves introducing a transgenic PDGF-C DM into a cell of a non-human animal, introducing the cell into a non-human animal and allowing the cell to develop into a non-human animal. The transgenic animal is useful as a model to study disease tattes characterised by over-expression of PDGF-C and to find therapy for those diseases, particularly hypertrophy and interest in various organis including the heart. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPLDLIANNAITARSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                            A transgenic animal over-expressing platelet derived growth factor Cuseful to study and find therapy for disease associated with PDGF-Cover-expression, including cardiac hypertrophy and fibrosis
                                          transgenic animal; platelet derived growth factor C; PDGF-C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 1858; DB 23; Length 345; 100.0%; Pred. No. 1.4e-179; cive 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                        Aase K,
                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 40-42; 48pp; English
                                                                                                                                                                                                                                       (LUDW-) LUDWIG INST CANCER RES
                                                          cardiac hypertrophy; fibrosis.
                                                                                                                                                                                                                                                                        Ponten A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is PDGF-C protein from human.
                                                                                                                                                                             28-MAR-2001; 2001WO-US09855.
                                                                                                                                                                                                         28-MAR-2000; 2000US-192507P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0
Matches 345; Conservative
                                                                                                                                                                                                                                                                                                   WPI; 2002-010700/01.
                                                                                                                                                                                                                                                                     Li X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       345 AA;
                                                                                                                  WO200172132-A1.
                                                                                      Homo sapiens
                                                                                                                                                04-OCT-2001
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LPLDLLINNALTAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL 240

GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA

LTEEVRLYSCTPRNFSVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300 

301 VIKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345 VIKKYHEVLQLRPKTGVRGLHKSLIDVALEHHEECDCVCRGSIGG 345

301

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AAY41766 standard; Protein; 345 AA.

RESULT 4

Human PRO200 protein sequence.

07-DEC-1999 (first entry)

AAY41766;

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VEGF-E; human; vascular endothelial cell growth factor; wound repair; treatment; cardiovascular disorder; endothelial disorder; therapy; tissue generation; regeneration; cardiac hypertrophy; cancer; detection; angiogenic disorder; age-related macular degeneration; vascular disease; neovascularization; tumor; gene mapping.
                                                                                                                                                                                                                                                        New growth factor polypeptide useful for treating cardiovascular or endothelial disorders, e.g. cardiac hypertrophy
                                                                                                                                                                                                                                                                                    Claim 1; Fig 2; 122pp; English,
                                                                                                                                                           99WO-US05190,
                                                                                                                                                                         98US-0040220.
                        11-JAN-2000 (first entry)
                                                                                                                                                                                                  (GETH ) GENENTECH INC
                                        Human VEGF-E protein
                                                                                                                                                                                                                                  WPI; 1999-580306/49.
                                                                                                                                                                                                                   Kuo SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        345 AA;
                                                                                                                                                                                                                                            N-PSDB; AAZ23691.
                                                                                                         Homo sapiens.
                                                                                                                         WO9947677-A2.
                                                                                                                                                           10-MAR-1999;
                                                                                                                                                                          17-MAR-1998;
                                                                                                                                                                                  02-NOV-1998;
                                                                                                                                          23-SEP-1999
                                                                                                                                                                                                                   Ferrara N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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This invention describes the isolation of a novel human vascular endothelial cell growth factor-E (VEGF-E) polypeptide which has tranquillizer, vulnery and cardiant activity. VEGF-E can be administered therapeutically, especially by expressing encoding polynucleotides, to treat cardiovascular or endothelial disorders in mammals, especially by mammals and tissue generation and may especially by expressing encoding polynucleotides, to treat cardiovascular or endothelial disorders in mammals, especially can be used to treat cardiac hypertrophy in can be combined with a carrier in pharmaceutical compositions, which regeneration, and may especially be used to treat dardinistered to can be administered to treat angiogenic disorders in mammals (especially humans) e.g. cancer or sereen for antagonists and agonists, and the antagonists administered to treat angiogenic disorders in mammals (especially them and the detect VEGF-E polypeptide, especially to disgnose cardiovascular, endothelial or angiogenic disorders in mammals (e.g. vascular disease, or neovascularization associated with tumor formation), by contacting the antibody with a tissue sample and detecting formation cardiovascular, polypeptide complex. Polymucleotides encoding VEGF-E can be used to disgnose cardiovascular and endothelial disorders in mammals, by detecting abnormally high or low VEGF-E gene expression in tissue samples. They can also be used to disgnose a disease or susceptibility to a disease related to a mutated form of VEGF-E can be used to produce probes useful to detect related semples. They may also be used to produce probes useful to detect related semples. They may also be used to produce probes useful to detect related semples. They may also be used to produce probes useful to detect related sequences or for gene mapping. This invention.
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99.4%; Pred. No. 7e-179;
Live 2; Mismatches 0; Indels 0;
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Matches 343; Conservative
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Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation; probe; blood coagulation disorder; cancer; cellular adhesion disorder; secreted protein; transmembrane protein.
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98US-0040220,
98US-0078886.
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                                                                  Homo sapiens
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12-MAR-1998;
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08-APR-1998;
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17-MAR-1998;
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26-MAR-1998;
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The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AA233891 to AA234338, and AAV1685 to AAV1774 represent polymucleotide and polypeptide sequence given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MSLFGLLLVTSALAGORRGTQAESNLSSKFQFSSNKEQNGVQDPQHERITTVSTNGSIHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vascular endothelial growth factor related protein; VEGF-R protein; tissue growth inhibition; tumour growth; cancer; tissue growth; angiogenesis; coronary artery blockage.
                                                                                                                                                                                                                                                                                                                                                             Query Match 99.6%; Score 1851; DB 20; Length 345; Best Local Similarity 99.4%; Pred. No. 7e-179; Matches 343; Conservative 2; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIXKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345
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Growth factor homologs and the nucleic acids that encode them, use of for treating liver damage, ischemia, multiple sclerosis and

e.g. for treating 11 Alzheimer's disease

Sheppard PO, Gilbertson DG;

03-MAY-2000; 2000WO-US40047.

10-NOV-1999; 99US-0164463. 04-FEB-2000; 2000US-0180169.

(ZYMO ) ZYMOGENETICS INC. Hart CE,

WPI; 2000-687541/67.

Gilbert T,

N-PSDB; AAC81582

99US-0304216

03-MAY-1999;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                MSLFGLLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS
                                                                                                                                                 related (VEGF-R) protein. VEGF-R can be used in assays to identify compounds that bind to it or that antegonize its activity. VEGF-R antagonizes (e.g. anti-VEGF-R antibodies) are useful for inhibiting tissue growth. This is useful for inhibiting tumour growth and for treating cancer. VEGF-R itself can be used to stimulate tissue growth, anglogenesis and to treat coronary artery blockage. The VEGF-R coding sequence can be used for the recombinant production of the VEGF-R protein.
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                                                         growth factor related protein and related for identifying antagonists and binding
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                                                                                                                                                                                                                                                                                                                               Length 345;
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Pred. No. 7e-179;
2; Mismatches 0; Indels
                                                                                                                                                The present sequence represents a vascular endothelial related (VEGF-R) protein. VEGF-R can be used in assays
                                                                                                                 Claim 1; Page 56-58; 62pp; English.
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                                                                                                                                                                                                                                                                                                                          99.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunomodulation; hepatic.
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Matches 343; Conservative
                                                          A vascular endothelial polynucleotide, useful
               1999-458680/38
                                                                                                                                                                                                                                                                                                  345 AA;
                             N-PSDB; AAX86352
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                                                                                        compounds
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The invention relates to the human growth factor homologue zvegf4

(AAB48653), and nucleic acids encoding it (AAC81555). Zvegf4 is a member

of the PoDGF (platelet-derived growth factor)/VEGF (vascular endothelial

growth factor) family. Zvegf4 has a growth factor domain (AAB48654)

characterised by a PDGF cystine knot structure, and a CUB domain

characterised by a PDGF cystine knot structure, and a CUB domain

characterised by a PDGF cystine knot structure. Zvegf4 has PDGF-like

activity, having mitogenic activity on fibroblasts, vascular smooth

comparisons a beta barrel structure. Zvegf4 has PDGF-like

activity, having mitogenic activity on fibroblasts, vascular smooth

comparisons expression constructs and host cells comprising human zvegf4

comparisons; expression constructs and host cells comprising human zvegf4 or fragments thereof, particularly human zvegf4 human zvegf4 and and post cells comprising human zvegf4 and and post cells comprising human zvegf4 or a fragment thereof; a method of activating

complete acids; the recombinant expression of human zvegf4; an antibody

complete complete pDGF receptor using a zvegf4-derived polypeptide; a

coll-surface PDGF receptor using a zvegf4-derived polypeptide; a

coll-surface PDGF receptor using a zvegf4-derived polypeptide; a

comprising exposing bone cells, comprising exposing bone cells to

compression of modulating the proliferation, differentiation, migration or

collular differentiation or proliferation. They are particularly used for cellular differentiation or proliferation. They are particularly used for multiple sclerosis). Due to their osteogenic activity, they may be used to

complete neurity growth (e.g., in the treatment of periodontal disease and fractures. They may be used to

complete sclerosis). Due to their osteogenic activity, they may be used to

complete colerosis or expected the colline colline colline colline sclerosis). The present cells, which may be used to used to enhance expansion and mobilisation of hamacopositic stem cells

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                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 48; Page 125-126; 143pp; English.
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Best Local Similarity
Matches 343; Conserv
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09-NOV-2000

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us-09-852-209a-3.rag

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AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic
LPLDLIANNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL
                241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK
                                                                                                                                                                                                                                                                                                                         Human, secreted protein; transmembrane protein, PRO; EST; cytostatic; expressed sequence tag, detection; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KF, Botstein D, Desnoyers L, Eaton DL;
E, Fong S, Gao W, Gerber H, Gerritsen ME;
PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
Napier MA, Pan J, Paoni NF, Roy MA;
TA, Tumas D, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel PRO polypeptides and polynucleotides used in detection metle
to target bioactive molecules to specific cells, and to modulate
                                                                                                                             301 VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG
                                                                                                                                                                                                                                                                                                Human PRO200 (UNQ174) protein sequence SEQ ID NO:488.
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                                                                                                                                                                                                                AAB44322 standard; Protein; 345
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99US-0134287.
99US-0141037.
99US-0145698.
99US-0162506.
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2000WO-US00277.
2000WO-US00376.
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99US-0126773.
99US-0130232.
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lvaroff E,
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Godowski PJ,
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cellular activities -
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06-JAN-2000;
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Goddard A,
Kljavin IJ,
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26-JUL-1999
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30-DEC-1999
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       LIBEVRLYSCIPRNFSVSIREELKRIDIIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a method for enhancing tissue growth, promoting wound healing or stimulating smooth muscle growth by administering a platelet-derived growth factor (PDGF) related protein, designated LPB or its analogue. Also described is a method of slowing the progress of atherosclerosis or treating atherosclerosis comprising the administration of an LPB antagonist. The method is useful for enhancing tissue growth, promoting wound healing and stimulating smooth muscle growth. Antagonists of LPB are useful for treating atherosclerosis. The present sequence represents human LPB, which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSLFGLLLVTSALAGQRRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enhancing tissue growth and promoting wound healing by administering platelet-derived growth factor related protein, LPB or its analog and treating atherosclerosis by administering LPB antagonist
                                                                                                                                                                                                                                           Human, platelet derived growth factor related protein, LPB; VEGFh; vascular endothelial growth factor h; tissue regeneration; vulnerary; atherosclerosis; PDGF-related protein; antiarteriosclerotic.
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                                                  301 VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345
                                 VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                  Human platelet-derived growth factor related protein LP8.
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Pred. No. 7e-179;
2; Mismatches (
                                                                                                                                  AAB24250 standard; Protein; 345 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 63-64; 64pp; English
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activity. The polymucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bioactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bioactive molecules to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
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                                                                                                                                                                                                                                                                                                               21; Length 345;
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                                                                                                                                                                                                                                                                                                         Score 1851; DB 21
Pred. No. 7e-179;
2; Mismatches 0
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                                                                                                                                                                                                                                                                                                            99.6%;
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Dhanaraj SN,
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                                                                                                                                                                            This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antiheumatic, antiarthritic, antipsoriatic and antidabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood and tissue repair in a subject. The products of the invention and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue repairs and account of the invention are useful pressure access.
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                                                                                        preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds
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                                                                       New vascular endothelial growth factor protein,
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Pred. No. 7e-179;
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                                                                                                                                              Disclosure, Fig 6, 127pp, English
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This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (1a) and its encoding polynucleotide (11a) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and antidabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood and tissue repair in a subject. The products of the invention and organ and tissue repairing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote
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venous sore; diabetic ulcer; burns; skin graft growth.
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99US-0124967.
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18-MAR-1999;
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Pred. No. 7e-179;
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N-PSDB; AAA71990.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBEVRLYSCIPRNFSVSIREELKRIDIIFWPGCLLVKRCGGNCACCLANCNECQCVPSK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 LTEEVRLYSCTPRNFSVSIRBELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
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for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity ovascularization. This sequence represents the human 990126vegx protein used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                          1 MSLFGLLLTTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 LPLDLINNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL
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                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                  Length 345;
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                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                  Score 1851; DB 21
Pred. No. 7e-179;
; Mismatches (
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                                                                                                                                                                                                                                                                                                  2;
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                                                                                                                                                                                                                                               99.6%;
ilarity 99.4%;
Conservative 2
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                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                              345 AA;
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08-NOV-1999;
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                                                                                                                                                                                                                                                                                                        Matches 343;
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Homo sapiens

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This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antisporiatic and antidiabetic activity and acts as an anglogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting anglogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ at the state growth, as ubject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graff growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents the human VEGF-X protein
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                                             preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                     growth factor protein, useful for treating
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Pred. No. 7e-179;
2; Mismatches 0; Indels 0
                                                                                                              Claim 72; Fig 12; 127pp; English.
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Best Local Similarity 99.4'
                        New vascular endothelial
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LIBEVALYSCIPPRNFSVSIREELKRIDIIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300 VIKKYHEVLQLRPKIGVRGLHKSLIDVALEHHEECDCVCRGSIGG 345 301 VTKKYHEVLQLRPKTGVRGLHKSLIDVALEHHEECDCVCRGSTGG 345 241 301 ď ð

LPLDLINNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL 240 LPLDLLINNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL 240

181 181 241

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AAB19578 standard; Protein; 345 AA (first entry) 22-JAN-2001 AAB19578; 

Human PRO200 (vascular endothelial growth factor E).

ocular disease; refinopathy; maculopathy; therapy; retinitis pigmentosa; macular degeneration; retinal detachment; retinal tear; macular bole; myopla; traumatic chorioretinopathy; acute retinal necrosis syndrome; contusion; dedma; retinal vision occlusion; vascular disease; retinal vasculitis; thrombocytopenic purpura; uveitis; retinal occlusion. PRO200; vascular epithelial growth factor E; VEGF-E; human;

Kabakoff RC; Henzel WJ, Wood WI; 25..29 /note= "Asn is N-glycosylated" 'note= "Asn is N-glycosylated" note= "Asn is N-glycosylated" Gurney AL, Hebert C, Kuo SS, La Fleur M, 282..288 /note= "N-myristoylation" 319..325 "N-myristoylation" "N-myristoylation" "N-myristoylation" "N-myristoylation" /label= Signal\_peptide /label= Mature\_Pro200 Location/Qualifiers /note= "Amidation" 10-MAR-2000; 2000WO-US06319. 99US-0123957. .133 ..123 254..258 281..287 /note= /note= 55..59 /note= /note= Goddard A, Kljavin IJ, (GETH ) GENENTECH INC WPI; 2000-587437/55. N-PSDB; AAA88515 WO200053760-A2 Modified-site Modified-site Modified-site Modified-site Modified-site Modified-site Modified-site Modified-site 12-MAR-1999; 14-SEP-2000 Ferrara N, Klein RD, Key Peptide Protein 

cells Novel PRO polypeptides useful for preventing or rescuing retinal cel from injury caused by ocular diseases such as retinitis pigmentosa, retinopathy, retinal degenerative diseases, degenerative myopia, uveitis

Claim 2; Fig 2; 140pp; English.

The present sequence is that of human PRO200 or vascular and other control factor E (VEGF-E), as predicted from a cDNA clone (see AAA88515) that was isolated from a glioma cell line G61 ilrary using probes (see AAA88521-26) based on an expressed sequence 1 ibrary using probes (see AAA88521-26) based on an expressed sequence comparison of 39,029 and a pi of about 6.06. A method for producing PRO polypeptides, including PRO200, using a host cell transformed with a vector comprising a PRO nucleic acid is claimed. The invanion relates to the use of PRO polypeptides to delay, prevent or rescue retinal cells such as retinal neurons selected from photoreceptors, retinal ganglion cells, displaced retinal again on cells, displaced amacrine cells, displaced including Mueller cells and photoreceptors and supportive cells (including Mueller cells and cells are preferably photoreceptors and depradation. The retinal cells from injury and degradation. The retinal cells from injury and degradation, retinal cells from injury and degradation, including age-related, retinal detachment, retinal degeneration, including age-related, retinal detachment, retinal cells and moular disease selected from retinal desenses, macular holes, degenerative myopia, acute relatal necrosis syndrome, traumatic chorioretinopathies or contusion such as Purtscher's retinal vision collagen vascular alseases, thrombocyclopenic purpura, celusion, collagen vascular as central or branch retinal vision uveits, retinal vasculitis and occlusion associated with Eales

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                                                                                                                                                                              GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA 180
                                                                                                                                                                                                                                                                        LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300
                                                                                                             MSLFGLLLLTSALAGORQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dermatological; antiarthriti; autithemmatic; immunosuppressive; haemostatic, antiarthriti; autithemmatic; immunosuppressive; haemostatic, antithyroid; autidiabetic; nootropic; neuroprotective; antiastamic; hepatotropic; virucide; antibsoriatic; antiallergic; antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; spondyloathropathy; systemic sclerosis; astroidosis; idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; autoimmune thrombocytopaenia; immune-mediated renal disease; demyelinating disease; hepatobiliary disease; Whipple's disease; demyelinating disease; immune-mediated skin disease; allergic disease; immune-mediated skin disease; allergic disease; immune-mediated skin disease; allergic disease; immune-mediated skin disease; allergic disease; graft rejection; graft-versus-host-disease.
                                                                                        1 MSLFGLLLVTSALAGQRRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS
                                                                  Gaps
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                                             Length 345;
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                                          Score 1851; DB 21; Length
Pred. No. 7e-179;
2; Mismatches 0; Indels
disease and systemic lupus erythematosus (claimed).
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990S-0123957.
990S-0125775.
990S-0128849.
99WO-US08615.
                                             99.6%;
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                                                      Local Similarity 99.4
les 343; Conservative
                      345 AA;
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12-MAR-1999;
23-MAR-1999;
12-APR-1999;
20-APR-1999;
28-APR-1999;
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Matches
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The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodise, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondybarthropathies, systemic ederosis, idiopathic inflammatory myopathies, sjographies, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune hrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demoyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases of the central and peripheral nervous systems, hepatobiliary diseases of the central count of immune-mediated skin diseases, allergic diseases, immunological disease, the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease.

AAC5837 to AAC58578 represent PCR primers and hybridisation probes used in the isolation of human PRO spolynucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus
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Pan J, Pennica D, Shelton DL, Smith V;
, Watanabe CK, Wood WI, Yan M;
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                     99US-0144758.
99US-0145698.
99US-0146222.
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Kabakoff RC, Lu Y, Pan J
Stewart TA, Tumas D, Wat
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-SUG6
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                                                                                                  01-SEP-1999;
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OY 1 MSLEGILLVTSALAGORRGTOARSKFORSSNKEONGVODPOHERITYSTNGSTHS 60
Db 1 INSLEGILLTSALAGORRGTOARSNLSSKFORSSNKEONGVODPOHERITYSTNGSTHS 60
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Db 61 PREPHTYPRNTYLVWRLYAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSGTIL 120
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OY 181 LPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL 240
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Db 301 VTKKYHBVLQLRPKTGVRGLHKSLTDVALEHHBECDCVCRGSTGG 345
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Search completed: November 25, 2003, 21:02:13 Job time : 36.9375 secs

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61 PRFPHTYPRNTVLVWRLVAVBENVWIQLTFDBRFGLBDPBDDICKYDFVEVEEPSDGTIL 120
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                                                                                                                                                                                               November 25, 2003, 21:04:39; Search time 24.3006 Seconds (without alignments) 2618.575 Million cell updates/sec
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| cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
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US-09-978-585A-488
US-09-978-191A-488
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ALIGNMENTS

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APPLICANT: ERIKSSON, U1f
APPLICANT: ERIKSSON, U1f
APPLICANT: L1, Xuxi
APPLICANT: L1, Xuxi
APPLICANT: L2, Xuxi
APPLICANT: L3, Xuxi
APPLICANT: AASE, Karin
APPLICANT: AASE, Karin
APPLICANT: L1, Hong
TITLE OF INVENTION: (POGF-C) AND USES THEREOF
FILE REFERENCE: 1064/4847
CURRENT APPLICATION NUMBER: US/09/818,943
CURRENT FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 60/192,507
PRIOR FILING DATE: 2000-03-28
NUMBER: OF SEQ ID NOS: 7
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100.0%; Score 1858; DB 9;
Best Local Similarity 100.0%; Pred. No. 3.1e-179;
Matches 345; Conservative 0; Mismatches 0;
; Sequence 1, Application US/09818943; Patent No. US20020049987A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin version 3.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
US-09-818-943-1
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241 LTEEVRLYSCTPRNFSVSIREELKRTDT1FWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300
                                                                                                                                                                                                            Sequence 32, Application US/10086623
Publication No. US20020164710A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                 APPLICANT: BRIKSSON, U1f
APPLICANT: AASE, Karin
APPLICANT: LI, Kuri
APPLICANT: PONTEN, Annica
APPLICANT: UUTELA, MARKO
APPLICANT: ALITALO, Kari
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ORGANISM: Homo sapiens
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US-10-086-623-32
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                                                                                241 LTEEVRLYSCTPRNFSVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300
LTEEVRLYSCTPRNFSVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300
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                                                           LPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL
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Best Local Similarity 100.0%; Pred. No. 3.1e-179;
Matches 345; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                         301 VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEBCDCVCRGSTGG 345
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APPLICANT: HELDIN, CATI-Henrik
APPLICANT: HELDIN, CATI-Henrik
APPLICANT: HEREDON, CATI-HEREDON
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,
TITLE OF INVENTION: THEREFOR, AND USES THEREOF
FILE REPREBRUE: 09-410.49-Eriksson et al-1064-44740
CURRENT APPLICATION NUMBER: US/09/852,209A
CURRENT APPLICATION NUMBER: 09/410,349
FRIOR FILING DATE: 1999-09-30
FRIOR FILING DATE: 1999-09-30
FRIOR APPLICATION NUMBER: 60/110,749
FRIOR APPLICATION NUMBER: 60/113,002
FRIOR FILING DATE: 1999-09-31
FRIOR FILING DATE: 1999-05-21
FRIOR FILING DATE: 1999-05-21
FRIOR FILING DATE: 1999-05-21
FRIOR FILING DATE: 1999-07-15
NUMBER: FLING DATE: 1999-07-15
NUMBER: FLING DATE: 1999-07-15
NUMBER: FLING DATE: 1999-07-15
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UUTELA, Marko
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OESTMAN, Arne
HELDIN, Carl-H
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LEE, Xuri
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:
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US-09-852-209A-3
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LENGTH: 345
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APPLICANT: OESTWAN, ARDER: APPLICANT: AREA APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: HELDIN, Carl-Henrik
TITILE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES 1
FILE REFERENCE: 1064/4483322
CURRENT APPLICATION NUMBER: US 60/107,852
PRIOR APPLICATION NUMBER: US 60/107,852
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 1999-10-04
PRIOR FILING DATE: 1999-10-04
PRIOR FILING DATE: 1999-10-04
PRIOR FILING DATE: 1999-11-0
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PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 09/438,046
PRIOR FILING DATE: 1999-11-10
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241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300
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; OTHER INFORMATION: Amino acid sequence for PDGF-C
US-10-086-623-32
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us-09-852-209a-3.rapb

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241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300
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                                                    301 VTKKYHEVLOLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345
                                                                                       VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345
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APPLICANT: OUTLAL, MAINE
APPLICANT: OCSTMAN, ARNE
APPLICANT: HELDIN, CARL'Henrik
APPLICANT: HELDIN, CARL'Henrik
APPLICANT: HELDIN, CARL'Henrik
TITLE OF INVENTION: THEREFOR, AND USES THEREOF
TITLE OF INVENTION: THEREFOR, AND USES THEREOF
TITLE OF INVENTION: THEREFOR, AND USES THEREOF
TILE REPERENCE: 09-410349-Eriksson et al-1064-44740
CURRENT PELING DATE: 1099-09-30
CURRENT APPLICATION NUMBER: US/09/410,349
PRIOR FILING DATE: 1999-09-30
PRIOR FILING DATE: 1998-11-12
PRIOR FILING DATE: 1998-10-03
PRIOR FILING DATE: 1998-12-03
PRIOR FILING DATE: 1998-12-13
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR FILING DATE: 1999-05-21
PRIOR PRING DATE: 1999-05-21
PRIOR PRING DATE: 1999-05-21
PRIOR FILING DATE: 1999-07-15
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100.0%; Pred. No. 3.1e-179;
ive 0; Mismatches 0;
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Publication No. US20030082670A1
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SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 100.0
Matches 345; Conservative
                                                                                                                                                                                                                                                                                                                                                               AASE, Karin
LEE, Xuri
PONTEN, Annica
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APPLICANT: ERIKSSON, Ulf
APPLICANT: AASE, Karin
APPLICANT: LEE, Kurin
APPLICANT: PONTEN, Annica
APPLICANT: UUTELA, Marko
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-600-3
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APPLICANT: UUTELA, MARKO

APPLICANT: UUTELA, MARKO

APPLICANT: ALITALO, KATI

APPLICANT: ALITALO, KATI

APPLICANT: CESTWAN, ATTEC

APPLICANT: CESTWAN, ATTEC

APPLICANT: CESTWAN, ATTEC

APPLICANT: HELDIN, CATI-HENTIK

TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES TH

FILE REFERRICE: 1064/44833C

CURRENT APPLICATION NUMBER: US/10/086,623

PRIOR APPLICATION NUMBER: US 60/107,852

PRIOR APPLICATION NUMBER: US 60/103,997

PRIOR APPLICATION NUMBER: US 60/103,604

PRIOR PILING DATE: 1999-10-04

PRIOR PILING DATE: 1999-10-04

PRIOR PILING DATE: 1999-10-04

PRIOR APPLICATION NUMBER: US 60/157,766

PRIOR APPLICATION NUMBER: US 60/157,766

PRIOR APPLICATION NUMBER: US 60/157,766

PRIOR APPLICATION NUMBER: US 60/157,766

PRIOR APPLICATION NUMBER: US 09/438,046

PRIOR APPLICATION NUMBER: US 09/438,046

PRIOR PILING DATE: 1999-11-0

PRIOR PILING DATE: 1999-11-0

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PRIOR PILING DATE: 1999-11-0

PRIOR PILING DATE: 1999-11-0

PRIOR PILING DATE: 1999-11-0

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PRIOR PILI
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                                                                                                        301 VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345
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OTHER INFORMATION: Amino acid sequence for PDGF-C
                                                                                                                                                                                                                                                      Sequence 32, Application US/10260539
Publication No. US20030073637A1
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UUTELA, Marko
ALITALO, Kari
OESTMAN, Arne
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LI, Xuri
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                Length 345;
                           Sequence 2, Application US/09823033
Patent No. US20020004225A1
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
TITLE OF INVENTION: LIGAMENT AND CARTILAGE
FILE REFERENCE: 00-12
CURRENT APPLICATION NUMBER: US/09/823,033
CURRENT APPLICATION NUMBER: US/09/823,033
CURRENT FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
ILENGTH: 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIKKYHEVLQLRPKTGVRGLHKSLTDVALEHHERCDCVCRGSTGG 345
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i Sequence 4, Application US/09923995

i Sequence 4. Application US/09923995

i Patent No. US2002008170081

i GENERAL INFORMATION:

i APPLICANT: Sheppard, Paul O.

I TITLE OF INVENTION: SNAKE VENOM POLYPEPTIDE ZSNK1

FILE REFERENCE: 00-47

CURRENT APPLICATION NUMBER: US/09/923,995

CURRENT FILING DATE: 2001-08-07

PRIOR FILING DATE: 2000-08-07

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                             Query Match 99.6%; Score 1851; DB 9;
Best Local Similarity 99.4%; Pred. No. 1.6e-178;
Matches 343; Conservative 2; Mismatches 0;
                                                                                                                                                                                                                                                 TYPE: PRT
CORGANISM: Homo sapiens
US-09-823-033-2
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ORGANISM: Homo sapiens
RESULT 6
US-09-823-033-2
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Length 345;

99.6%; Score 1851; DB 9; 99.4%; Pred. No. 1.6e-178;

Query Match Best Local Similarity

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                                                    1 MSLFGLLLVTSALAGQRRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS
                                                                                                      1 MSLFGLLLITSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS
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US-09-795-006A-149

i Sequence 149, Application US/09795006A

j Patent No. US20020151680A1

j GENERAL INFORMATION:

j APPLICANT Alitalo et al

i TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR

i TITLE OF INVENTION: ENDOTHELIAL GROWTH PACTOR DNAS AND PROFEINS

i TITLE OF INVENTION: ENDOTHELIAL GROWTH PACTOR DNAS AND PROFEINS

i TITLE OF INVENTION: ENDOTHELIAL GROWTH PACTOR DNAS AND PROFEINS

i CURRENT APPLICATION NUMBER: US 60/205, 331

j PRIOR APPLICATION NUMBER: US 60/205, 331

j PRIOR APPLICATION NUMBER: US 60/185, 205

j NUMBER OF SEQ ID NOS: 175

j SEQ ID NO 149

j ENGTH: 345
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2; Mismatches
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  343; Conservative
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Best Local Similarity 99.4
Matches 343; Conservative
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US-09-795-006A-149
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  Matches
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PELICANT: Nag-
APPLICANT: Pach, James,
APPLICANT: Pach, James,
APPLICANT: Pach, James,
APPLICANT: Pach, James,
APPLICANT: Scheart, Timothy A.
APPLICANT: Stevart, Timothy A.
APPLICANT: Thurs, Daniel
APPLICANT: Thurs, Daniel
APPLICANT: Thurs, Daniel
APPLICANT: Thurs, Daniel
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
ITITE OF INVENTION: Secreted and Transmembrane Polypeptides and Mucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Mucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: 1997-10-17-15
PRIOR PLILIANTON NUMBER: SO(077541
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PRIOR PLILIAND NUMBER: SO(077541
PRIOR PLILIAND NUMBER: SO(077541
PRIOR PLILIAND NUMBER: SO(07791)
PRIOR PLILIAND NUMBER: SO(079910
PRIOR PLILIAND NUMBER: SO(079910
PRIOR PLILIAND NUMBER: SO(079930
PRIOR PLILIAND NUMBER: SO(079930
PRIOR PLILIAND NUMBER: SO(079930
                           301 VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345
301 VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345
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3C-09-378-295A-488
; Sequence 488, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INPORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Borstein, David
; APPLICANT: Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
Fong, Sherman
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APPLICANT:
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APPLICANT:
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PRIOR APPLICATION NUMBER: 60/07956
PRIOR PILICATION NUMBER: 60/07966
PRIOR FILING DATE: 1936-03-26
PRIOR FILING DATE: 1936-03-26
PRIOR PLICATION NUMBER: 60/079663
PRIOR PLICATION NUMBER: 60/07967
PRIOR PLICATION NUMBER: 60/07928
PRIOR PELICATION NUMBER: 60/07928
PRIOR PELICATION NUMBER: 60/07923
PRIOR PELICATION NUMBER: 60/07923
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PRIOR PELICATION NUMBER: 60/080194
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PRIOR PELICATION NUMBER: 60/080196
PRIOR PELICATION NUMBER: 60/080196
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121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA 180
                                                                                          181 IPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL 240
                                                                                                                                                                                           241 LTEEVRLYSCTPRNFSVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300
                                                                                                                                                                                                                                                                                                                241 LTBEVALYSCTPRNFSVSIRBELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300
61 PRFPHTYPRNTVLVWRLVAVEENVWIQL/FDERFGLEDPEDDICKYDFVEVEFSDGTIL 120
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CURRENT APPLICATION NUMBER: U5/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/94885
PRIOR PELLING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 06/06220
PRIOR APPLICATION NUMBER: 06/064249
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-13
PRIOR PELLING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/06364
PRIOR APPLICATION NUMBER: 60/06364
PRIOR PELLING DATE: 1997-11-21
PRIOR PELLING DATE: 1997-11-21
PRIOR PELLING DATE: 1998-03-10
PRIOR PELLING DATE: 1998-03-10
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
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Patent No. US20020169284A1
GENERAL INFORMATION:
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Shelton, David L.
Stewart, Timothy A.
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Williams, P. Mickey
Wood, William I.
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Paoni, Nicholas F.
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Kuo, Sophia S.
Napier, Mary A.
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Eaton, Dan
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tive 2; Mismatches 0;
                                                                            PRIOR APPLICATION NUMBER: 60/083495
PRIOR PLING DATE: 1998-04-29
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1998-03-11 NUMBER: 60/07791 1998-03-12 NUMBER: 60/078004 1998-03-13 1998-03-20 NUMBER: 60/07886 1998-03-20 NUMBER: 60/078936 11998-03-20 NUMBER: 60/078936 11998-03-20 NUMBER: 60/078939	1998-03-25  NUMBER: 60/079656  NUMBER: 60/079664  NUMBER: 60/079689  1998-03-27  NUMBER: 60/079683  1998-03-27  NUMBER: 60/079786  1998-03-27  NUMBER: 60/079786  1998-03-27  NUMBER: 60/07920  1998-03-27  NUMBER: 60/07920  NUMBER: 60/07920  1998-03-31  NUMBER: 60/080107  1998-03-31  NUMBER: 60/080165  1998-03-31  NUMBER: 60/080327  1998-03-31  NUMBER: 60/080328  1998-03-31  NUMBER: 60/080333  1998-04-01  NUMBER: 60/080333  1998-04-01  NUMBER: 60/080333  1998-04-01  NUMBER: 60/080333	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                     1 MSLFGLLILTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS
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                                                                                               Length 345;
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                                                                                                                                                               0; Indels
                                                                                               Query Match 99.6%; Score 1851; DB 10;
Best Local Similarity 99.4%; Pred. No. 1.6e-178;
Matches 343; Conservative 2; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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Sequence 488, Application US/09978192A
Patent No. US2002017553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
      PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
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Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerriteen, Mary E.
Goddard, Audrey
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Paoni, Nicholas F.
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Desnoyers, Luc
Eaton, Dan
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R RAPELICATION NUMBER: 60/078936
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R APPLICATION NUMBER: 60/079294
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R FILING DATE: 1998-03-11
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R APPLICATION NUMBER: 60/077649
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APPLICATION NUMBER: 60/081955
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                        FILING DATE: 1997-11-03
APPLICATION NUMBER: 60/065311
FILING DATE: 1997-11-13
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APPLICATION NUMBER: 60/077450
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APPLICATION UNMBER: 60/077791
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APPLICATION NUMBER: 60/078004
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APPLICATION NUMBER: 60/079664
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APPLICATION NUMBER: 60/078886
APPLICATION NUMBER: 60/064249
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Best Local Similarity 99.4%; Pred. No. 1.6e-178;
Matches 343; Conservative 2; Mismatches 0;
          PRIOR FILING DATE: 1998-05-15
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PRIOR FILING DATE: 1998-05-15
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PRIOR APPLICATION NUMBER: 60/085573
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Grimaldi, J. Christopher
APPLICATION NUMBER: 60/085582
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Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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Filvaroff, Ellen
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Gerritsen, Mary E.
Goddard, Audrey
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Eaton, Dan
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Gao, Wei-Qiang
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US-09-999-832A-488
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Paoni, Nicholas F. Roy, Margaret Ann Shelton, David L.

APPLICANT: APPLICANT: APPLICANT:

Pan, James

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APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PLGS.

CURRENT APPLICATION NUMBER: US/09/999,832A

CURRENT FILING DATE: 2001-10-24
                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2001-10-24

PRIOR APPLICATION NUMBER: 09/918585

PRIOR APPLICATION NUMBER: 06/064249

PRIOR APPLICATION NUMBER: 06/064249

PRIOR APPLICATION NUMBER: 06/064311

PRIOR APPLICATION NUMBER: 06/065311

PRIOR APPLICATION NUMBER: 06/065311

PRIOR PILING DATE: 1997-10-31

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FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080333
APPLICATION NUMBER: 60/080334
FILING DATE: 1998-04-01
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William I.
   APPLICANT:
APPLICANT:
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PRIOR APPLICATION NUMBER: 60/081049
PRIOR PELLING DATE: 1998-04-08
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APPLICANT: Thumas, Daniel
APPLICANT: Thumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2650911C7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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PRIOR FILING DATE: 2001-07-30
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Pan, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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RAPPLICATION NUMBER: 60/084600

R APPLICATION NUMBER: 60/084627

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R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/085339

R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/085339

R FILING DATE: 1998-05-13

R APPLICATION NUMBER: 60/085323

R FILING DATE: 1998-05-13

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Publication No. US20030004102A1
GENERAL INFORMATION:
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Oiang
Gerber, Hanspeter
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Baton, Dan
APPLICANT: Baton, Dan
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Best Local Similarity 99.44
Matches 343; Conservative
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R FILING DATE: 1998-04-21

R APPLICATION NUMBER: 60/082704

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R APPLICATION NUMBER: 60/082797

R FILING DATE: 1998-04-22

R APPLICATION NUMBER: 60/082796

R FILING DATE: 1998-04-23

R APPLICATION NUMBER: 60/08136

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R APPLICATION NUMBER: 60/08332

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R FILING DATE: 1998-04-28

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R APLING DATE: 1998-04-29
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          TON NUMBER: 60/080165
ATE: 1998-03-31
          APPLICATION NUMBER: 60/080165
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APPLICATION NUMBER: 60/080194
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FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083500
APPLING DATE: 1998-04-29
APPLICATION NUMBER: 60/083742
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PRIOR PLING DATE: 1998-05-05
PRIOR PLING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/08441
PRIOR PLING DATE: 1998-05-06
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                                                                           JENBEAL INFURMALION:
APPLICANT: MCCATCHY, Sean A.
APPLICANT: MCCATCHY, Sean A.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-227-99
CURRENT APPLICATION NUMBER: US/09/796,753
CURRENT FILING DATE: 2001-03
PRIOR APPLICATION NUMBER: 09/183,175
PRIOR FILING DATE: 1998-10-30
PRIOR FILING DATE: 1998-10-30
PRIOR FILING DATE: 1998-12-30
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PRIOR APPLICATION NUMBER: 09/223,546
PRIOR PELING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/224,246
PRIOR PELING DATE: 1998-02-02
PRIOR PELING DATE: 1999-03-01
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PRIOR FILING DATE: 2000-09-30
NUMBER OF SEQ ID NOS: 162
Sequence 6, Application US/09796753 Publication No. US20030027998A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.4%
Matches 343; Conservative
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630PIC22
CURRENT APPLICATION VUMBER: US/09/978,608A
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624
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301 VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345
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LENGTH: 345
                                                                                                               Sequence 488, Application US/09978608A Publication No. US20030045462A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Williams, P. Mickey Wood, William I.
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Filvaroff, Ellen
Fong, Sherman
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Shelton, David L.
Stewart, Timothy A.
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Gerritsen, Mary E.
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Kljavin, Ivar J.
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Desnoyers, Luc
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Best Local Similarity 99.4'
Matches 343; Conservative
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APPLICANT: Baker Kevin P.
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                                                                                            US-09-978-608A-488
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APPLICANT:
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345	VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG
LHNCNECQCVPSK 300	LTEEVRLYSCTPRNFSVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK
LHNCNECQCVPSK 300	LTBEVRLYSCTPRNFSVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK
	LPLDLINNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL
VFGRKSRVVDLNL 240	LPLDILINNAITAFSTLEDLIKYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL
	GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSYLPPSA
TEAVSPSVLPPSA 180	GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA
	PRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEBPSDGTIL
FVEVEEPSDGTIL 120	PRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTIL

Search completed: November 25, 2003, 21:17:04 Job time : 25.3006 secs

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GenCore version 5.1.6
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```

OM protein - protein search, using sw model

Run on:

November 25, 2003, 20:59:34; Search time 14.7173 Seconds (without alignments) 2254.373 Million cell updates/sec

US-09-852-209A-3 1858 1 MSLFGLLLVTSALAGQRRGT.....DVALEHHEECDCVCRGSTGG 345 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STRMMARTES

		•			SUMMARIES	
Result No.	Score	* Query Match	* Query Match Length	DB	ID	Description
	1111111			-	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	!
-	742.5	40.0	370	0	JC7591	
7	736	ď	370	~	JC7592	spinal cord-derive
m	183		3623	~	T09456	intrinsic factor-B
4	8		730	Н	BMHU1	procollagen C-endo
ស	179.5	•	927	,-1	JQ0948	AS antigen precurs
ø	176	9.5	707	~	JC2218	procollagen C-endo
7	176		3623	~	T08618	intrinsic factor-B
80	173		823	г	A58788	procollagen C-endo
6	169	9.1	986	П	B58788	procollagen C-endo
10	169	9.1	991	~	I49540	ပ်
11	154	8.3	449	N	A55362	procellagen I C-pr
12	148.5	8.0	1057	Н	A39288	2
13	143.5	7.7	686	~	A59271	
14	139.5	•	1070	7	T31069	tolloid-BMP-1 like
15	138.5	7.5	597	C3	871352	metalloproteinase
16	138	7.4	705	Н	CIHURB	complement subcomp
17	137.5	7.4	669	Н	I54763	ű
18	137.5		1524	~	T30337	polyprotein - Afri
19	133	7.2	1594	N	T30549	hensin - rabbit
20	132		419	N	869207	vascular endotheli
21	130.5	7.0	1464	7	S58984	14
22	128	6.9	402	N	JH0403	procollagen I C-pr
23	127.5	٠	767	N	T30018	
24	127.5	6.9	3871		T22812	hypothetical prote
25	125	•	198		JS0735	•••
26	123.5		277	~	A41735	•~
27	123.5	9.9	579		JC7629	membrane-type friz
28	120.5	-:	245	Н	-	ved
29	120.5	6.5	275	0	JC6506	tumor necrosis fac

TSG-6 homolog PS4	platelet-derived g	platelet-derived g	platelet-derived g	platelet-derived g	UVS.2 protein - Af	sanko - human	platelet-derived g	platelet-derived g	PDGF-related trans	platelet-derived g	vascular endotheli	platelet-derived g	platelet-derived g	protein F57C12.1 [
A47290	PFHUG2	151551	S08220	IS1550	I51569	A59386	JN0248	325096	TVMVSS	A37359	A41551	B28964	PFHUG1	D89447
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376	241	200	215	226	319	2403	166	197	226	196	232	196	211	170
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	 9					5.9						5.6	5,6	5.5
4.0		6.1	6.1	6.1	0.9		5.9	5.9	5.8	8.8	5.6		104 5.6	5.5

## **ALIGNMENTS**

SULT	1					
7591						
inal	cord-derived	growth	factor-B	h factor-B precursor	1	hun

Cispecies: Homo sapiens (man)
Cibate: 30-Unn-2001 #text\_change 24-Aug-2001
Cibate: 30-Unn-2001 #sequence\_revision 30-Jun-2001 #text\_change 24-Aug-2001
Cibate: 30-Unn-2001 #sequence\_revision 30-Jun-2001 #text\_change 24-Aug-2001
Cibate: 30-Unn-2001 #sequence\_revision 30-Jun-2001 #text\_change 24-Aug-2001
Cibate: 30-Unn-2001 #text\_change 24-Aug-2001
A; Hitle: Molecular cloning of SCDGF-B, a novel growth factor homologous to SCDGF/PDGF-A; Reference number: JC7591; MUID:21092670; PMID:11162582
A; Molecule type: DNA
A; Residues: 1-370 < HAM>

A; Cross-references: DDBJ:AB033832

A; Gene: scdgf-B F;1-17/Domain: secretory signal sequence #status predicted <SIG> F;18-370/Product: spinal cord-derived growth factor-B #status predicted F;52-170/Region: CUB domain #status predicted F;272-370/Region: homologous to platelet-derived growth factor/vascular endothelial gr F;294-308/Region: conserved motif #status predicted

Query Match
40.0%; Score 742.5; DB 2; Length 370;
Best Local Similarity 43.6%; Pred. No. 9e-57;
Matches 159; Conservative 59; Mismatches 114; Indels 33; Gaps

59 HSPRFPHTYPRNTVLVWRLVAVEENVWIQLIFDERFGLEDPEDDICKYDFVEVEEPSDGT 118 3 LFGLLLVTSALAGQRRGTQAESNLSSKFQFSSN---KEQNGVQD-PQHERIITVSTNGSI 58 S IFVYTLICANFCSCRDTSATPOSASIKALRNANLRRDESNHLTDLYRRDETIQVKGNGYV 64 g à g ò

119 --ILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAV---- 171 ð

172 -----SPSVLPPSALPLDLLNNAITAFSTLEDLIRYLEPERWOLDLEDLYR 217 183 WESVTSSISGVSYNSPSVTDPT-LIADALDKKIAEPDTVEDLLKYFNPESWQEDLENMYL 241 요 ò g

218 PTWOLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLV 277 Š 셤

278 KRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRP---KTGVRGLHKSLTDVALEHHEE 334 300 QRCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTWALVDIQLDHHER 359 ઠે g

CDCVC 339 335 ( à 23;

950

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A; Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen ty C; Superfamily: procollagen C-endopeptidase; astacin homology; Clr/Cls repeat homology; Cs/Superfamily: procollagen C-endopeptidase; astacin homology; Clr/Cls repeat homology; F; 23-730/Promain: signal sequence #seatus predicted <signal-azi/Domain: signal sequence #seatus predicted (signal) = 1310-321/Domain: satacin homology <a href="Asi30-321/Domain: Clr/Cls repeat homology">AST> F; 32-431/Domain: Clr/Cls repeat homology</a> <a href="Asi30-321/Domain: Clr/Cls repeat homology">ClR1> F; 531-700/Domain: Clr/Cls repeat homology</a> <a href="Asi30-359/Binding">ClR2> F; 531-700/Domain: Clr/Cls repeat homology</a> <a href="Asi30-359/Binding">ClR2> F; 531-700/Domain: Clr/Cls repeat homology</a> <a href="Asi30-559/Binding">ClR2> F; 531-300/Domain: /a> site: carbohydrate (Asi) (covalent) #status predicted F; 133-217, 233, 272/Binding site: zinc (His, His, Tyr) #status predicted F; 231, 217, 233, 227, 251-567, 251-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567, 551-567,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            951 VYPHGINCTWHIL-VQPNHLIHLMF-ETFHLEFHYN--CTNDYLEVYDTDSETSLGRYCG 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1100 G-NYYTDFLEIRDGGYEKSPLLGIFYGSNLPPTIISHSNKLWLKFKSDQIDTRSGFSAYW 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------YPNNW----ECIYRITVRTGQLIAVHFINFSLEEAI 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1159 DGS--STGCGCN----LTTSSGTFISPNYPMPYYHSSECYWWLKSSHG-SAFELEFKDFH 1211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 SGTVPGKQISKGNQIRIRFVSDEYFPSBPGFCIHYNIV-----MPQFTEAVSPSVLPPS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272 PGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHE---VLQLRPKTGVRGLHKSLTDVA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form BMP1 - huma N;Alternate names: bone morphogenic protein 1 (BMP1)
C;Species: Homo sapiens (man)
C;Dete: 16-Sep-1992 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
C;Accession: A37278; E56788
R;Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz Science 242, 1528-1534, 1988
A;Title: Novel regulators of bone formation: molecular clones and activities. A;Reference number: A37278; MUID:88072730; PMID:3201241
                                                                                                                                                                                                                                                                                                                                                                                                66 TYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 GTQAESNLSSKFQF----SSNKEQNG-----VQDPQHERIITVSTNGSIHSPRFPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 ALPLDLLNNAITAFSTLEDLIRYLEPERWOLDLEDLYR---PTWOLLGKAFVFGRKSRVV
                                                                                                                                                                                                                                                                                          Gaps
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A;Cross-references: GB:M22488; NID:g179499; PIDN:AAA51833.1; PID:g179500
                                                                                                                                                                                                                                                                                      90;
C; Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology C; Keywords: receptor; vitamin B12 uptake F;1-24/Domain: signal sequence #status predicted <SIG> F;1-24/Domain: signal sequence #status predicted <SIG> F;25-3623/Product: intrinsic factor-B12 receptor #status predicted F;436-467/Domain: EGF homology <EGF>
                                                                                                                                                                                                                    Length 3623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 DINLLTE--EVR-------LY--SCTPRNFSVSIREELK-RTDTI-
                                                                                                                                                                                                         9.8%; Score 183; DB 2; Length 36;
6.2%; Pred. No. 8.2e-07;
ve 42; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GDB:125203; OMIM:112264
A; Map position: 8p21-8p21
C; Function:
                                                                                                                                                                                                                                              26.2%;
                                                                                                                                                                                                                                                                                  96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1063 ----NFPNN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          329 LEHHEEC 335
                                                                                                                                                                                                                                                     Similarity
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Best Local (
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Matches
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18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>
52-170/Region: CUB domain #status predicted
;272-370/Region: homologous to platele
                                                                                                                                                                                                                                                                                                                                                                                         to SCDGF/PDGF-C/
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C;Species: Homo sapiens (man)
C;Date: 16-U1-1999 #sequence_revision 16-Jul-1999 #text_change 02-Aug-2002
C;Accession: T109456
R;Kozyraki, R.; Kristiansen, M.; Silahtaroglu, A.; Hansen, C.; Jacobsen, C.; Tommerup,
Blood 91, 3593-3600, 1998
A;Title: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular character:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 ESNHLTDLYRRDENIRVTGTGHVQSPRFPNSYPRNLLLTWRLHS-QEKTRIQLAFDHQFG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Reference number: Z16677; MUID:98241400; PMID:9572993
A)Accession: T09456
A)Status: preliminary; translated from GB/EMBL/DDBJ
A)MOLecule type: mRNA
A;Residues: 1-3623 <ROZ>
A;Cross-references: EMBL:AF034611; NID:g3929528; PIDN:AAC82612.1; PID:g3929529
C;Genetics:
A;Map position: 10p12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --SPSVLPPSALPLDLLNNAITAFST 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEDPEDDICKYDFVEVEEPSDGT--ILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEDLIRYLEPERWOLDLEDLYRPTWOLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNF 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95
                                                                                                                                                         Spinal cord-derived growth factor-B precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 24-Aug-2001
C;Accession: JC7592
R;Hamada, T.; Ui-Tei, K.; Imaki, J.; Miyata, Y.
Biochem. Biophys. Res. Commun. 280, 733-73, 2001
A;Fitle: Molecular cloning of ScOGF-B, a novel growth factor homologous to SC
A;Contents: Fetal brain
A;Reference number: JC7591; MUID:21092670; PMID:11162582
A;Contents: Fetal brain
A;Accession: JC7592
A;Molecule type: mRNA
A;Accession: JC7592
A;Molecule type: mRNA
A;Accession: JC7592
A;Molecule type: mRNA
A;Cross-references: DDBJ:AB052170
C;Genetics:
F;1-17/Domain: secretory signal sequence #status predicted <SIG>F;1-17/Domain: secretory signal sequence drowth factor-B #status predicted
F;1-17/Domain: secretory signal status predicted
F;272-170/Region: Conserved motif #status predicted
F;294-308/Region: conserved motif #status predicted
                                                                                                                                                                                                  Species: Rattus norvegicus (Norway rat)
Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 24-Aug-2001
Accession: JC7592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 39.6%; Score 736; DB 2; Best Local Similarity 45.6%; Pred. No. 3.3e-56; Matches 149; Conservative 57; Mismatches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -KTGVRGLHKSLTDVALEHHEECDCVC 339
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C.Superfamily: intrinsic factor-B12 receptor cubilin; BGF homology
C;Keywords: egg yolk; endocytosis; glycoprotein; intestine; kidney; peripheral membran;
F;1-20/Domain: signal sequence #status predicted <SIG>
F;1-20/Bowain: signal sequence #status predicted <SIG>
F;133-164/Domain: BGF homology <BGF!>
F;133-164/Domain: BGF homology <BGF>
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A;Title: The intrinsic factor-vitamin Bl2 receptor and target of teratogenic antibodies A;Reference number: 216459; MUID:98148073; PMID:9478979
                        A;Title: Cloning and expression of CDNA encoding Xenopus laevis bone morphogenetic prol
A;Reference number: JC2218; MUID:94085787; PMID:8262384
A;Accession: JC2218
                                                                                                                                                                                                                                                                                                      Cycomment: This protein induces ectopic cartilage formation in vivo.
Cysuperfamily: procollagen C-endopeptidase; astacin homology; Clr/Cls repeat homology;
Cysuperfamily: procollagen C-endopeptidase; astacin homology; Clr/Cls repeat homology; Cls/Cls repeat homology sAST>
F;285-394/Domain: astacin homology sAST>
F;285-394/Domain: Complement Ir/Is-like repeat
F;389-510/Region: complement Ir/Is-like repeat
F;389-510/Region: complement Ir/Is-like repeat
F;389-507/Domain: Clr/Cls repeat homology sCIR2>
F;554-666/Region: complement Ir/Is-like repeat
F;554-666/Region: complement Ir/Is-like repeat
F;554-666/Region: complement Ir/Is-like repeat
F;654-666/Region: complement Ir/Is-like repeat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: EMBL; AF022247; NID: 93834379; PIDN: AAC71661.1; PID: 93834380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intrinsic factor-B12 receptor CUBILIN precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 02-Aug-2002
C;Accession: T08618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;528/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
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                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-707 <MAE>
A;Cross-references: GB:L12249; NID:9406540; PIDN:AAA16313.1; PID:9406541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.5%; Score 176; DB 2; Length 3623; 25.5%; Pred. No. 3.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 707;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    618 LTSDSKLHCKFCCS-ELPAVITSQYNNMRIEPKSDNTV-SKKCF 659
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Matches 95; Conservative 52; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.5%; Score 176; DB 2; 43.3%; Pred. No. 4.2e-07;
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A; Status: preliminary; translated from GB/EMBL/DDBJ
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Gene 134, 257-261, 1993
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JOOGA8
A5 antigen precursor - African clawed frog
C; Species: Xenopus laevis (African clawed frog)
C; Species: Xenopus laevis (African clawed frog)
C; Species: Xenopus laevis (African clawed frog)
C; Species: Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C; Accession: JH0466; JOOG48
R; Takagi, S.; Hirata, T.; Agata, K.; Mochii, M.; Eguchi, G.; Fujisawa, H.
Neuron 7, 295-307, 1991
A; Title: The A5 antigen, a candidate for the neuronal recognition molecule, has homologi
A; Reference number: JH0466; MUID:91337458; PMID:1908252
A; Residues: 1-927 - TAK>
A; Residues: 1-927 - TAK>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 EV--EEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCHYNIVMP-- 165
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                                                                                                                                                                                                                                                                                  55 NGSIHSPREPHTYPRNTVLVWRLVA-VEENVWIQLTFDERFGLEDPEDDICKXDFVEVEE 113
                                                                                                                                                                                                                                                                                                                                                                            599 NGSITSPGWPKEYPPNKNCIWQLVAPTQYRISLQFDFFETEG-----NDVCKYDFVEVRS 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 --PSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 IKITSPSYLTSAGXPHSYPPSQRCEWLIQAPEHYQRIMINFNPHFDLEDRE---CKYDYV 87
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         F;565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
                                                                                                                                                                                             17; Gaps
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                                                                                    ch 9.8%; Score 181.5; DB 1; Length 730; 1 Similarity 37.3%; Pred. No. 1.4e-07; 50; Conservative 20; Mismatches 47; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.7%; Score 179.5; DB 1; Length 9
31.6%; Pred. No. 2.9e-07;
tive 29; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 SPSVLPPSALPLDL 185
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A; Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen ty C; Superfamily: procollagen C-endopeptidase; astacin homology; Cir/Cis repeat homology; C; Superfamily: procollagen C-endopeptidase; astacin homology; Cir/Cis repeat homology; C; Sylvayacds: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; F; 12-22/Domain: signal sequence #status predicted <SiG.>
F; 23-986/Product: procollagen C-endopeptidase tolloid-like splice form #status prediction; F; 32-431/Domain: Cir/Cis repeat homology <CiR1>
F; 532-431/Domain: Cir/Cis repeat homology <CiR2>
F; 551-587/Domain: Cir/Cis repeat homology <CiR3>
F; 551-700/Domain: Cir/Cis repeat homology <CiR3>
F; 707-742/Domain: Cir/Cis repeat homology <CiR4>
F; 747-856/Domain: Cir/Cis repeat homology <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.W.; H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F,860-973/Domain: Cir/Cis repeat homology <CLRS>
F)91,142,322.363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted
F)163-319,185-205,322-348,375-397,431-461,488-510,551-563,559-572,574-587,591-617,644-F;213,217,223,2729.Binding site: zinc (His, His, His, Tyr) #status predicted
F;214/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                         - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-702, EKRPALQPPRGRPHQLKFRVQKRNRTPQ' <WOZ>
A; Cross-references: GB:M22488; NID:g179499; PIDN:AAA51833.1; PID:g179500
R; Takahara, K.; Lyons, G.E.; Greenspan, D.S.
R; Takahara, C. Se9, 32572-32578; 1994
A; Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld) are A; Reference number: A58788; MUID:95096114; PMID:7798260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;565,720/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2
                                                                                                                                                                                                                                                                                                                                                                                                                                     splice form
        --PSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDBYFPSEPGFCIHYNIVMPQFTEAV 171
                                                                         654 GLTADSKLHGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGFKAHFFSVLEGAGDRH 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M.J.; Kriz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 NGSIHSPRFPHTYPRNTVLVWRLVA-VEENVWIQLTFDERFGLEDPEDDICKYDFVEVEE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                 procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice for N;Alternate names: bone morphogenic protein 1, tolloid-like splice form C;Species: Homo sapiens (man)
C;Date: 28-Mar.1998 #sequence_revision 09-Apr.1998 #text_change 16-Jul-1999 C;Accession: A37278; BS8788
R;Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kri Science 242, 1528-1534, 1988
A;Title: Novel regulators of bone formation: molecular clones and activities A;Reference number: A37278; MUID:89072730; PMID:3201241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 703-986 <TAK>
A;Cross-references: GB:L3S279; NID:g619860; PIDN:AAC41710.1; PID:g619861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 169; DB 1; Length 986;
Pred. No. 2.6e-06;
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                                                                                                                                                                                                                                         SHLSGLELLLCPHALVDTVPAPPSAL 737
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A;Cross-references: GDB:125203; OMIM:112264
A;Map position: 8p21-8p21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A37278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: B5878
                                                                                                                                                               172
                                                                                                                                                                                                                                         712
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Matches
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Alcession: A3728, A5878

Richard and a sequence revision 09-Apr-1998 #text_change 18-Jun-1999

Cipate: 28-Mar-1998 sequence revision 09-Apr-1998 #text_change 18-Jun-1999

Cipate: 28-Mar-1998 sequence revision 09-Apr-1998 #text_change 18-Jun-1999

Cipate: 28-Mar-1998 sequence revision 09-Apr-1998 #text_change 18-Jun-1999

Cipate: 28-Mar-1998 sequence revision 09-Apr-1998 #text_change 18-Jun-1999

Cipate: 28-Mar-1998 sequence revision 09-Apr-1998 #text_change 18-Jun-1999

Cipate: 28-Mar-1998 sequence revision 09-Apr-1998 #text_change 18-Jun-1999

Richard A1728, A58788 MUD198072730; PMID1301841

A) Received: A3728, MUD189072730; PMID1301841

A) Residuce: Richard A1728, MUD189072730; PMID1301841

A) Residuce: Richard A1728, MUD189072730; PMID1301841

A) Received: Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipate Cipat
1059 LSSPNFPNNYPSNWECIYRITVGLNQQIALHFTDF-TLEDYFGSQCVDFVB------IR 1110
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                                                                                                                                                                                                                                                                              DLYRPTWQLLGKAFVFGRKSRVVDLNLLTEEVRLY-----SCTPRNFSVSIREELKRT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                     267 DTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHE---VLQLRPKTGVRGLHKS 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGSIHSPRFPHTYPRNTVLVWRLVA-VEENVWIQLTFDERFGLEDPEDDICKYDFVEVEE 113
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35.6%; Pred. No. 9.2e-07;
iive 19; Mismatches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1207 FODFHLEHHPSC 1218
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                                                                                                                  SVLP--PSALPLDL.
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Best Local Similarity
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C;Species: Homo sapiens (man)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 16-Jun-2000
C;Accession: A59271
R;Thiel, S.; Vovup-Jensen, T.; Stover, C.M.; Schwaeble, W.J.; Laursen, S.B.; Poulsen, S.Mature 386, 506-510, 1997
Asture 386, 506-510, 1997
A;Title: A second serine protease associated with mannan-binding lectin that activates A;Reference number: A59271; MUID:97242412; PMID:9087411
                                                                                                                                                                                                                                                                                                                                                                                                                                     dorsal-ventral patterning protein tolloid (EC 3.4.24.-) - fruit fly (Drosophila melano C; Species: Drosophila melanogaster
C; Species: Drosophila melanogaster
C; Species: Drosophila melanogaster
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: A33288
R; Shimell, M.J.; Ferguson, E.L.; Childs, S.R.; O'Connor, M.B.
A; Shimell, M.J.; Ferguson, E.L.; Childs, S.R.; O'Connor, M.B.
A; Title: The Drosophila dorsal-ventral patterning gene tolloid is related to human bon A; Reference number: A39288; MUID:92034970; PMID:1840509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               parts of this sequence, including the amino end of the mature protein, were del
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N/Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)
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224 AVSDDSRRLGKFCGD-AVPGSISSEGNELLVQFVSDLSVTAD-GFSASYK-TLPRGTAKE 280
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A;Residues: 1-686 <JEN>
A;Across-referemes: GR:Y09926; NID:g4007626; PIDN:CAA71059.1; PID:g4007627
A;Experimental source: tissue liver
A;Note: submitted to GenBank, December 1996
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18.0%; Pred. No. 0.00017;
                                                                                                            169 -----EAVSPSV-LPPSALP 182
                                                                                                                                                                                                             281 GOGPGPKRGTEPKVKLPPKSQP 302
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Best Local Similarity 38.0%;
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A;Molecule type: mRNA
A;Residues: 1-1057 <SHI>
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R;Takahara, K.; Kessler, E.; Biniaminov, L.; Brusel, M.; Eddy, R.L.; Jani-Sait, S.; Show
Biol. Chem. 269, 26280-26285, 1994
A;Title: The I procollagen COOH-terminal proteinsee enhancer protein: identification, p
A;Reference number: A55362; MUID:95014462; PMID:7523404
A;Accession: A55362
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A; Map position: 7421.3-7422
C; Superfamily: Cir/Cis repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 EEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFT--- 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 NGSIHSPRFPHTYPRNTVLVWRLVA-VEENVWIQLTFDERFGLEDPEDDICKYDFVEVEE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             604 NGSITSPGWPKEYPPNKNCIWQLVAPTQYRISLQFDFFFTEG-----NDVCKYDFVEVRS 658
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C;Species: Homo sapiens (man)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 05-Nov-1999
          C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
9.1%; Score 169; DB 2; Length 991;
Best Local Similarity 39.4%; Pred. No. 2.6e-06;
Matches 43; Conservative 17; Mismatches 39; Indels 10; Gaps
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A; Residues: 1-449 <TAK>
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A;Gene: GDB:PCOLCE
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Best Local Similarity 24.4%
Matches 59; Conservative
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Colloid-BMP-1 like protein 1 - California sea hare
tolloid-BMP-1 like protein 1 - California sea hare
Cispecies: Aplysia californica (California sea hare)
Cispecies: Aplysia californica (California sea hare)
Cispecies: Aplysia californica (California sea hare)
Cispecies: Aplysia californica (California sea hare)
Cispecies: Aplysia californica (California sea hare)
Cispecies: Aplysia californica (California sea hare)
Cispecies: Tall69
Talla: Ascession: Tall69
Alfile: A developmental gene (Tolloid/BMP-1) is regulated in Aplysia Neurons by treatme
Algebrance number: Z20965; MUID:98007484; PMID:8987797
Alfile: A developmental gene (Tolloid/BMP-1) is regulated in Aplysia Neurons by treatme
Algebrance number: Z20965; MUID:98007484; PMID:89807797
Algebrance: Trpe: mRNA
Algebrance: Informative translated from GB/EMBL/DDBJ
Algebrance: Informative translated from GB/EMBL/DDBJ
Algebrance: EMBL:U57369; NID:91899041; PID:91899042; PIDN:AAC47485.1
Cisperfamily: dorsal-ventral patterning protein tolloid; astacin homology; CIr/CIs repe
A;Map position: 1p36.2-lp36.3
C;Superfamily: complement subcomponent Clr; Clr/Cls repeat homology; complement factor H
C;Reywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serine F
C;Reywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serine F
F;1-15/Domain: signal sequence #status predicted <SIG>F;16-444,445-686/Product: Ra-reactive factor 2 #status predicted <MAT>
F;19-134/Domain: Clr/Cls repeat homology <CIR1>
F;142-180/Domain: BGF homology <EGF>F;142-180/Domain: Clr/Cls repeat homology <CIR2>
F;184-233/Domain: complement factor H repeat homology <FH1>
F;366-410/Domain: complement factor H repeat homology <FH2>
F;366-410/Domain: trypsin homology <TRY>
F;445-679/Domain: trypsin homology <TRY>
F;12-90,142-156,152-180,184-211,241-259,300-348,328-361,366-412,386-430,434-552, F;158/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F;444-445/Cleavage site: Arg-1le (autolytic) #status predicted
F;483,522,633/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 NGSIHSPRPPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVERP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQL---TFDERFGLEDPEDDICKYDFVEVE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 LPPSALPLDLLNNAITARS-----TLEDLIRYLEPERWQLDLEDLYRPTWQLLGKARVFG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YPPD------EXXCVWHISAPKGHTLTVNFTHMDLE-WRGDECEL-----DFVRVTNVVG 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----NIVMPQFTEAVSPSV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           640 DHGCEHVCVNTLGSYECTCKIGYELHSDGKKCEKACGGYLDAPSGTISSPSF----PDL 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 RKSRVVDLNLLTEEVRLYSCTPRNFSVS--IREELKRTDTIFWPGCLL-----VKRCGGN 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               742 NKER-----LOGOYCGFWAPPSITSLSNELRIBFRSDDTLOKTGFSMDYVADVDECASS 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 686;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 SDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHY 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.5%; Score 139.5; DB 2; larity 21.9%; Pred. No. 0.0011; Conservative 36; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                    7.7%; Score 143.5; DB 1
32.1%; Pred. No. 0.00027;
tive 25; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        284 CACCLHNCN-----ECQC 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Best Local Similarity (
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es 70; Conserv
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A)Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-7, S',9-10, V',12-28, H',30-72, 'D',74-77,'SK',80-81,'I',83-232,'R',234-2
A;Residues: 1-7, S',9-10, V',12-28, 'H',30-72,'D',74-77,'SK',80-81,'I',83-232,'R',234-2
B-571,'N',573-584,'D',586-595,'D',597 <LBP>
A;Cross-references: ERMBL:X5624; NID:g10929
A;Experimental source: embryo
A;Note: sequence extracted from NCBI backbone (NCBIP:99979)
            - sea urchin (Paracentrotus liv
metalloproteinase (BC 3.4.24.-) 10 precursor, blastula - sea urchin (Paracentrotus liv NyAlernate names: gene tolloid protein homolog C; Species: Paracentrotus lividus (common urchin) C; Date: 12-Feb-1998 #sequence revision 13-Mar-1998 #text_change 17-Mar-1999 C; Accession: S71352; A44880; S22060 E; Liepage, T.; Gache, C. Bur. J. Blochem. 238, 744-751, 1996 A; Title: Structure of the gene encoding the sea urchin blastula protease 10 (BP10), a M; Reference number: S71352; MUID:96300240; PMID:8706676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RiLepage, T.; Ghiglione, C.; Gache, C. Development 114, 147-163, 1992
A;Title Spatial and temporal expression pattern during sea urchin embryogenesis of a A;Teterning gene tolloid.
A;Reference number: A44880; MUID:92249197; PMID:1339338
                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-597 cLHO>
A;Residues: 1-597 cLHO>
A;Cross-references: EMBL:X65721; NID:e956534; PID:e46942
A;Experimental source: sperm
A;Note: the authors translated the codon GCT for residue 11 as Val, AAC for residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVITSPNWPGRYDDNMACVYQIEGPPGST-IELTFTE---MNIENHAVCRYDAVEIRKDD 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --SDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                459 TTTI-STTTPVPTTTQATTDETVVGSCGGRFGGTQGRVATPNY--PNNYDNDL/CVYVIE 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --AFSTLEDLI---RYLEPERWQLDLEDLYRPT 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 WQLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKR 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---IDMKM 556
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F;339-446/Domain: Clr/Cls repeat homology <CIRI>
F;349-292/Domain: Clr/Cls repeat homology <CIRI>
F;404-292/Domain: Clr/Cls repeat homology <CIRI>
F;190,194,200/Shinding site: zinc (His) #status predicted
F;191/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Introns: 30/3; 116/1; 184/3; 252/3; 370/3; 555/2
C;Superfamily: Clr/Cls repeat homology; astacin homology
C;Keywords: hydrolase; metalloproteinase; zinc
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-597/Product: metalloproteinase 10, blastula #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92;
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57

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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 25, 2003, 20:55:48; Search time 8.55655 Seconds (without alignments) 1896.117 Million cell updates/sec Run on:

US-09-852-209A-3 1858 1 MSLFGLLLVTSALAGQRRGT.....DVALEHHEECDCVCRGSTGG 345 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	١×		stron	7	3 mus m	060462 homo sapien	Q9qwj9 rattus norv	035276 rattus norv	1 ratt	mus	ß	O57460 brachydanio	homo s	gallı	Q15113 homo sapien	drose	homo	рошо	ย ธาพ	P42674 paracentrot	P98064 mus musculu	stron		h con		mus m		7 oryc	mus m	5 homo 8	Felis	ō	P98065 oryctolagus
SUMMARIES	םו	RP	BMP1 XENLA	SPAN STRPU	BMP1 HUMAN	BMP1 MOUSE	NRP2 HUMAN	NRP1 RAT	NRP2 RAT			NRP2_MOUSE	TLD BRARE	NRP1_HUMAN	NRP1 CHICK	PCO1 HUMAN	TLD DROME	VEGD HUMAN	MAS2_HUMAN	VEGD_MOUSE	BP10_PARLI		BMPH STRPU	C1R_HUMAN	CRAR_HUMAN	VEGC HUMAN	PCO1_MOUSE	PCO1_RAT	PDGA_RABIT	VEGC_MOUSE	TSG6 HUMAN	PDGB_FELCA	TSG6_MOUSE	TSG6_RABIT
	DB		~	Н	٦	ч	Н	н	Н	~	<b>,-</b> 4	H	Н	н	Н	Н	П	٦	Н	-	-	7	H	-	-	7	н	Н	Н	-1	Н	Н	Н	н
	Length	i i	707	616	986	166	931	922	925	326	923	931	1022	923	914	449	1057	354	989	358	597	704	639	705	669	419	468	468	213	415	277	245	275	276
	% Query Match	9.7	9.5				8.0				8.6	•	8.6	8.5	•		8.0		7.7		٠	•	7.4	٠	•	٠		•	6.7	•	9.9	•	6.5	6.4
	Score	179.5	176	173.5	169	169	164.5	ë.	w	162.5		•	TU.	158.5	157	154	148.5	147	143.5	140	139.5	138.5	138	$\rightarrow$	137.5	132	128	128	125	-	123.5	120.5	120.5	118.5
	Result No.		7	e	4	വ	9	7	æ	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	59	30	31	32	33

P52585 orf virus ( P01127 homo sapien	P13698 xenopus lae	P42664 xenopus lae	P20033 mus musculu	P28576 rattus norv	P26617 cavia porce	P01128 simian sarc	P49765 homo sapien	P15692 homo sapien	P04085 homo sapien	P52584 orf virus (
VEGH ORFN7	PDGA_XENLA	UVS2_XENLA	PDGA_MOUSE	PDGA_RAT	VEGA CAVPO	TSIS_SMSAV	VEGB HUMAN	VEGA HUMAN	PDGA HUMAN	VEGH_ORFN2
٦.	٦	ч	Н	rt	~1	~1	Н	Н	н	н
148	226	514	211	204	164	226	207	232	211	133
2.5	6.1	6.0	5,9	5.9	5.8	5. 8.	5.7	5.6	5.6	5.5
114.5	112.5	111.5	110	109	108.5	108.5	105.5	104.5	104	102.5

## ALIGNMENTS

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7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 ITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 EV--EEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMP-- 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 ----OFTEA--VSPSVLPPSALPLDLINNAITAFSTLEDLIRYLEPERWQLDLE 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 ECSRNFTSSNGVIKSPKYPEKYPNALBCTYIIFAPKOQEIV--LEFESFELEAD 197
                                                                                                                    Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maeno M., Xue Y., Wood T.I., Ong R.C., Kung H.F.;
"Cloning and expression of cDNA encoding Xenopus laevis bone
morphogenetic protein-1 during early embryonic development.";
Gene 134:257-261(1993)
-!- FUNCTION: INVOLVED IN PATTERN FORMATION IN GASTRULA AND LATER
DIFFERENTIATION OF DEVELOPING ORGANS.
-!- DEVELOPMENTAL STAGE: BLASTULA, EARLY GASTRULA AND HATCHED
TADPOLES; LITTLE OR NO EXPRESSION IN WORULA AND LATE GASTRULA.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996 (Rel. 33, Created)
20-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bone morphogenetic protein 1 precursor (EC 3.4.24.-) (BMP-1).
Renopus laevis (African clawed frog).
Eukaryota; Metazoa; Choordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 BY SIMILARITY.
584 BY SIMILARITY.
150 N-LINKED (GLCNAC. .) (POTENTIAL).
300 N-LINKED (GLCNAC. .) (POTENTIAL).
523 N-LINKED (GLCNAC. .) (POTENTIAL).
524 N-LINKED (GLCNAC. .) (POTENTIAL).
103416 MW; AF6B323BOA4C789D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.7%; Score 179.5; DB 1; Length 928;
31.6%; Pred. No. 2e-07;
ive 29; Mismatches 73; Indels 17;
                                                                                                                                                                                            NEUROPILIN-1.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                          F5/8 TYPE C 1.
F5/8 TYPE C 2.
MAM.
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                                                                                                                                                                       POTENTIAL
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MEDLINE=94085787; PubMed=8262384;
PS01285; FA58C_1; 2.

PS01286; FA58C_2; 2.

PS00725; FA58C_3; 2.

PS00740; MAM_1; 1.

PS50060; MAM_2; 1.
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Conservative 2
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NCBI_TaxID=8355;
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844
828 AA;
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                                                                                                                                                  Receptor; Antigen.
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22
861
884
27
147
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P98070;
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  PROSITE;
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                                                                                                    PROSITE;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lb.sib.ch).
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EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
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N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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SINC (CATALYTIC) (BY SIMILARITY)
ZINC (CATALYTIC) (BY SIMILARITY)
ZINC (CATALYTIC) (BY SIMILARITY)
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43.3%; Pred. No. 2.9e-07;
tive 15; Mismatches 36,
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-!- SIMILARITY: Contains 1 BGF-like domain.
-!- SIMILARITY: Contains 3 CUB domains.
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MEROPS, M12.005; ...
InterPro; IRR00156; Astacin.
InterPro; IRR00156; Astacin.
InterPro; IRR00159; GUB domain.
InterPro; IRR00181; EGF Ca.
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PROSITE; PS00010; ASX HYDROXYL; 1.
PROSITE; PS00022; BGF 1; PALSE NEG-PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01187; EGF CA; 1.
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SIGNAL
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                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=92315921; Pubmed=1618141;
Reynolds S.D., Angerer L.M., Palis J., Nasir A., Angerer R.C.;
Reynolds S.D., Angerer L.M. Falis J., Nasir A., Angerer R.C.;
"Early mRNAs, spatially restricted along the animal-vegetal axis of sea urchin embryos, include one encoding a protein related to tolloid
                                                                                                                      Strongylocentrotus purpuratus (Purple sea urchin).
Bukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euechinoidea, Echinacea, Echinoida, Strongylocentrotidae,
                                                                                                                                                                                                                                                                                                PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; PALSE NEG.
Developmental protein; Repeat; Hydrolase; Protease; Zinc; Embryo; Metalloprotease; EGF-like domain; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY)
(BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARG/LYS-RICH (BASIC).
                                                                                                                                                                                                                                                                                                                                                                 AND MAICHTEST.
-! SIMILARITY: BELONGS TO PERTIDASE FAMILY ML2A.
-!- SIMILARITY: Contains 1 BGF-like domain.
-!- SIMILARITY: Contains 2 CUB domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZINC (CATALYTIC)
BY SIMILARITY.
ZINC (CATALYTIC)
ZINC (CATALYTIC)
                                                 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
SPAN protein precursor (EC 3.4.24.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METALLOPROTEASE
                           616 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; ITR001506; Astacin.
InterPro; ITR000559; CUB domain.
InterPro; ITR000529; CUB domain.
InterPro; ITR000520; EGF like.
InterPro; ITR006020; IGGF like.
InterPro; ITR006020; IGGF like.
InterPro; ITR006020; IGGF like.
InterPro; ITR006020; IGGF like.
Ffam; PF00431; CUB; 2.
Ffam; PF00431; CUB; 2.
SMART; SM00181; EGF; 1.
SMART; SM00181; EGF; 1.
PROSITE; PS00142; ZINC PROTEASE; 1.
PROSITE; PS01180; CUB; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGF-LIKE.
                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M84144; AAA30072.1; -.
                           STANDARD;
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                                                                                                                                                                    Strongylocentrotus.
                                                                                                                                                                                                                                                                                                                                                           AND HATCHING)
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                                                                                                                                                                                     NCBI TaxID=7668;
                                                                                                                                                                                                                                                                                      BMP-1.";
                           SPAN STRPU
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RESULT 3
SPAN_STRPU
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510 VEGRVASPNY------PNDYDNSLQCDYVIEVDDGRRVELIFEDFGLEDETTCRW 558
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                                                                                                                                                                                                                                                        116 DGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPS--EPGFCIHYNIVMPQFTEAVSP 173
                                                                                                                                                                                                                                                                                 405 INSIGEKECGN-TLPPVQISSSNOMMVSFTSD---PSITRRGFKATYVIII-QTTTVFST 459
                                                                                                                                                                                                                                                                                                                                    174 SVL---PPSALPLDLLNNAITAFSTLEDLIRYLEPERWOLDLEDLYRPTWOLLGKAFVFG 230
                                                                                                                                                                                                                                                                                                                                                                          460 TILQITPPSITILQITNPSITILQI-----TNPSITILQITD--TPVIGSCGGTFV-G 509
                                                                                                                                                                                                                                                                                                                                                                                                                  231 RKSRVVDLNLLTEEVRLYSCTPRNFSVSIR-----EELKRIDTIF------W 271
                                                                                                                                                                                                                349 GEITSPNYPSNYEDNTACVYBIEGPYGST-IELTF---LDMEIBTETLCRYDAVEVRKDD 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Janitz M., Heiser V., Boettcher U., Landt O., Lauster R.;
"Three alternatively spliced variants of the gene coding for the human
bone morphogenetic protein-1";
J. Wol. Med. 76:141-146(1998).
                                                                                                                                      63; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The C-proteinase that processes procollagens to fibrillar collagens is identical to the protein previously identified as bone morphogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMP1 HUMAN STANDARD;
PRI; 986 AA.
PRI397, Q1392; Q13972; Q19421; Q99422; Q99423; Q9UL38;
PRI3497, Q1392; Q13972; Q1874; Q99421; Q99422; Q99423; Q9UL38;
16-OCT-2001 (Rel. 40, Last sequence update)
28-FRB-2003 (Rel. 41, Last annocation update)
Bone morphogenetic protein 1 precursor (EC 3.4.24.19) (BMP-1)
(Procollagen C-proteinase) (PCP) (Mammalian tolloid protein) (MTld).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wozney J.M., Rosen V., Celeste A.J., Mitsock L.M., Whitters M.J., Kriz R.W., Hewick R.M., Wang E.A.; "Novel regulators of bone formation: molecular clones and
                                                                                                DB 1; Length 616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li S.W., Sieron A.L., Fertala A., Hojima Y., Arnold W.V., Prockop D.J.;
                                                                                                                                    70; Conservative 33; Mismatches 93; Indels
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BY SIMILARITY.

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397CD923FFB9EB98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 93:5127-5130(1996).
                                                                                                9.3%; Score 173.5; DB 1
27.0%; Pred. No. 3.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM BMP1-1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96209868; PubMed=8643539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89072730; PubMed=3201241;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  272 PGCLL------VKRCG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        559 DSLMINLGNGIKVGMKMCG 577
  299 315 BY
305 317 BY
319 328 BX
616 AA; 67902 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 242:1528-1534(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Placenta;
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  DISULFID
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                                                                                                       Query Match
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    Takahara K., Lyons G.B., Greenspan D.S.;
"Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld)
are encoded by alternatively spliced transcripts which are
differentially expressed in some tissues.";
J. Blol. Chem. 269:32572-32578 (1994).
                                                                                                                                               MEDINE 21336528; PubMed=11289002;

Garrigue-Antar L., Barker C., Kadler K.B.;

"Identification of amino acid residues in bone morphogenetic

"Identification of amino acid residues in bone morphogenetic

"Identification of procollagen C-proteinase activity.";

J. Biol. Chem. 276:26237-26242(2001).

-!- FUNCTION: CIEAVES THE C-PERMINAL PROPEPTIDES OF PROCOLLAGEN I, II

-!- FUNCTION: CIEAVES THE C-PERMINAL PROPERTION.

-!- CATALITIC ACTIVITY: Cleavage of the C-terminal propeptide at

Ala-|-Asp in type I and II procollagens and at Arg-|-Asp in type
                                                                                                                                                                                                                                                                                                                                        -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
-!- ENZYME REGULATION: ACTIVITY IS INCREASED BY THE PROCOLLAGEN C-
ENDOPEPTIDASE ENHANCER PROTEIN.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INCLEDENTIA 97-6; Sequence=VSP 005469, VSP 005470; ISSUE SPECIFICITY: Ubiquitous.
--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
--- SIMILARITY: Contains 2 EGF-like domains.
--- SIMILARITY: Contains 5 CUB domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=P13497-2; Sequence=VSP_005461, VSP_005462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=P13497-3; Sequence=VSP_005463, VSP_005464;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM; 112264; ---
GO; GO:0005576; C:extracellular; NAS.
GO; GO:000577; F:metallopeptidase activity; NAS.
GO; GO:0001502; F:metallopeptidase activity; NAS.
GO; GO:0001502; F:cartilage condensation; TAS.
InterPro; IPR001502; Astacin.
InterPro; IPR001801; Astacin.
InterPro; IPR001801; Astacin.
InterPro; IPR001801; Astacin.
InterPro; IPR001801; Astacin.
InterPro; IPR006039; GGF_like.
InterPro; IPR006026; NZn_WTpeptdse.
InterPro; IPR006025; Zn_WTpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=BMP1-2;
Isold=P13497-7; Sequence=Not described;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=P13497-1; Sequence=Displayed;
                                                                                                                                   DISULFIDE BOND IN METALLOPROTEASE DOMAIN.
MEDLINE=95096114; PubMed=7798260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, U50330; AAA93462.1; BMBL, M22489; AAA51833.1; BMBL; V08723; CAA69973.1; BMBL; Y08725; CAA69975.1; BMBL; Y08725; CAA69975.1; BMBL; L35278; AAC41703.1; BMBL; A37278; BS8788. BIRSP, P07736; IAPQ. MEROPS; M12.005; CAR
                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=BMP1-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=BMP1-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=BMP1-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=BMP1-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=BMP1-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=BMP1-7
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DKDECSKDNGGCQQDCVNIFGSYECQCR -> EKRPALQPP
RGRPHQLKFRVQKRNRTPQ (in isoform BMP1-1).
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IVPKYEVNGVKPPIGQR -> VLASSLLLLSCGSRNGASFP
CSLESSTHQALCWTGLFLRPSPFPRLPLAAPRTLRAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> GCY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
CUB 4.
CUB 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DKDECSKDNGGCQQD -> GGELFGLLGHPPRRP (in isoform BMP1-6).
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/FIId=VSP 005463.
Missing (in isoform BMP1.4).
/FIId=VSP 005464.
AAGGGFLTKLMCSITSFGWPKEYPPNKNCIWQLV -
DLQVGKPLLWDRHCFRLSTHGPEMLGTALRG (in
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(BY SIMILARITY)
                                                                                                                                                                                                                              PROSITE, PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00180; CUB; 5.
PROSITE; PS00101 ASX HYDROXYL; 2.
PROSITE; PS00102; EGF_1; FALSE_NEG.
PROSITE; PS001186; EGF_2; 2.
Growth factor; Cytokine; Repeat; Bone; Cartilage; Hydrolase; Metalloprotease; EGF-like domain; Zinc; Calcium; Signal; Glycoprotein; Zymogen; Alternative splicing.

Glycoprotein; Zymogen; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Missing (in isoform BMP1-6).
/FTId=VSP_005468.
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Missing (in isoform BMP1-5).
/FTId=VSP_005466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BONE MORPHOGENETIC PROTEIN METALLOPROTEASE.
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ZINC (CATALYTIC)
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SMART; SM00179; EGF CA; 2.
SMART; SM00235; ZnMc; 1.
Pfam, PF01400; Astacin; 1. Pfam; PF00431; CUB; 5. Pfam; PF00008; EGF; 2. PRINTS; PR00480; ASTACIN.
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                 VKLTFMEMDIESQPECAYDHLEVFDGRDAKAPVLGRFCG
--> VLDGADDRHSHUSGLELLLCHPHLVDVFDAPBAGAIGGD
--> THAHTHTWITHCPIAQETCRGPPLGASRLSPQGPGHLTLA
PQEGSYLDFWDTHRGDPKPRRRKSLKTFSLTPATFRGIWA
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MEDLINE=94229142; PubMed=8174772;
Pukagawa M., Noborus S., Hogan B.L.M., Jones C.M.;
Fukagawa M., Noborus S., Hogan B.L.M., Jones C.M.;
Fukagawa M., Noborus S., Hogan B.L.M., Jones C.M.;
Which is related to the Drosophila dorsoventral gene tolloid and encodes a putative astacin metalloendopeptidase.";
Dev. Biol. 163:175-183(1994).
-1- FUNCTION: CLEAVES THE C-TERMINAL PROPEPTIDES OF PROCOLLAGEN I, II AND II. INDUCES CAPRILAGE AND BONE FORMATION.
-1- CATALYTIC ACTIVITY: Cleavage of the C-terminal propeptide at Ala-|-Asp in type and II procollagens and at Arg-|-Asp in type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1. COFACTOR: Binds 1 zinc ion per subunit (By similarity).
-1. ENZYME REGULATION: ACTIVITY IS INCREASED BY THE PROCOLLAGEN C-ENDOPERTIDASE ENHANCER PROTEIN.
-1. TISSUE SPECIFICITY: AT HIGH LEVELS IN EMBRYONIC MATERNAL DECIDIUM AND FLOOR PLATE REGION OF THE NEURAL TUBE. LESS IN DEVELOPING MEMBRANOUS AND THE MESENCHYME OF SPIEEN AND LUNG.
-1. SIMILARITY: BELONGS TO PEPTIDASE FAMILY MIZA.
-1. SIMILARITY: CONTAINS 5 CUB domains.
EAGCDHKVTSTSGTITSPNWPDKYPSKKECTWAISSTPGHR
                                                                                                                                                                                                                                                                                                                                             39; Indela 10; Gaps
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Ol-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bone morphogenetic protein 1 precursor (EC 3.4.24.19) (BMP-1)
(Procollagen C-proteinase) (PCP) (Mammalian tolloid protein) (mTld).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 --PSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSBPGFCIHY 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           654 GLTADSKLHGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGFKAHF 700
                                                                                                                                                                                                                                                                                           Length 986;
                                                                                                       L (in lecform EMP1-7).

F/FTIG=VSP 005469.

824 986 Missing (in isoform BMP1-7).

FTIG=VSP 005470.

748 748 D -> N (IM REF. 4).

934 934 R -> S (IN REF. 4).

986 AA, 111248 MW, F89201913AC3CBEA CRC64;
                                                                                                                                                                                                                                                                                                1 9.1%; Score 169; DB 1; Similarity 39.4%; Pred. No. 1.7e-06;
                                                                                                                                                                                                                                                                                                                                               17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 991 AA
                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                               43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BMP1 MOUSE
P98063;
                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                              VARSPLIC
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                                                                                                                                                                                                            CONFLICT
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55 NGSIHSPRFPHTYPRNTVLVWRLVA-VEENVWIQLTFDERFGLEDPEDDICKYDFVEVEE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
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19.4%; Pred. No. 1.7e-06;
lve 17; Mismatches 39; Indels 10; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PSO0142; ZINC_PROTEASE; 1.
PROSITE; PSO0140; ZINC_PROTEASE; 1.
PROSITE; PSO0140; ASX_HYDROXYL; 2.
PROSITE; PSO0180; BGF 1; FALSE_NEG.
PROSITE; PS01186; EGF 2; 2.
PROSITE; PS01187; EGF CA; 2.
PROSITE; PS01187; EGF CA; 2.
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ZINC (CATALYTIC) (1)
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InterPro; IPR006205; EGF like.
InterPro; IPR006205; EGF like.
InterPro; IPR006025; Zn MTpeptdse.
Pfam; PF01400; Astacin; 1.
Pfam; PF00431; CUB; 5.
Pfam; PR00408; EGF; 2.
PRINTS; PR00480; ASTACIN.
SWART; SW00179; EGF CA; SWART; SW00179; EGF CA; SWART; SW00179; EGF CA; CAMER; SW00179; EGF CA; CAMER; SW00179; EGF CA; CAMER; SW00135; ZnMG; 1.
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                                                                                  MEROPS; mis.v...
MEROPS; mis.v.s.
MEROPS; B8176; Bmpl.
InterPro; IPR001506; Astacin.
InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR000859; CUB Gomain.
EMBL; 124755; AAA37306.1; -. PIR; 149540; 149540.
HSSP; P00736; 1APQ.
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SIGNAL 1 25
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X MEDLINE-20309748; PubMed=10748121;
A Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;
Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;
Gluzman-Poltorak Z., Cohen T. Herzog Y., Neufeld G.;
T "Neuropilin-2 and neuropilin-1 are receptors for the 165-amino acid form of vascular endothelial growth factor (VEGF) and of placenta growth factor-2, but only neuropilin-2 functions as a receptor for the 145-amino acid form of VEGF.";
J. Biol. Chem. 275:18040-18045(2000).
- PUNCTION: HIGH APFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165 AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.
- SUBNIXI: NEUROPILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH CHARLY LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS A0 AND A17).
MEDLINE-97470888; PubMed=9331348;
Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;
"Neuropilin-2, a novel member of the neuropilin family, is a high
affinity receptor for the semaphorins Sema E and Sema IV but not Sema
                                                                                                                                                                                                 NRP2 HUMAN STANDARD; PRT; 931 AA.
060462; 014821;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
18-FBB-2003 (Rel. 41, Last annotation update)
Neuropilin-2 precursor (Vascular endothelial cell growth factor 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soker S., Takashima S., Miao H.-Q., Neufeld G., Klagsbrun M.; "Neuropilin-1 is expressed by endothelial and tumor cells as an isoform-specific receptor for vascular endothelial growth factor."; Cell 92:735-745(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
659 GLIADSKLHGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGFKAHF 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISOIG=060462-3; Sequence=VSP_004341;
-!- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
-!- SIMILARITY: Contains 2 CUB domains.
-!- SIMILARITY: Contains 2 F5/8 type C domains.
-!- SIMILARITY: Contains 1 MAM domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event-Alternative splicing; Named isoforms=3;
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Isold=O60462-1; Sequence=Displayed;
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EMBL; AF022860; AAC51789.1; -.
EMBL; AF016098; AAC12922.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neuron 19:547-559(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor 2).
NRP2 OR VEGF165R2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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61 PRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVE--EPSDGT 118
MIM; 602070; -.

GO; GO:0005624; F:receptor activity; TAS.

GO; GO:0004872; F:receptor activity; TAS.

GO; GO:0004872; F:receptor activity; TAS.

GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; TAS.

GO; GO:0007411; P:axon guidance; TAS.

InterPro; IPR000829; PAB domain.

InterPro; IPR00098; MAM domain.

Pfam; PP00431; CUB; 2.

Pfam; PP00529; MAM; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSLFGLLLVTSALAGQRRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
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N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
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SMART; SM000231; FASEC; 2.
SMART; SM00137; MAM; 1.
PROSITE; PS01286; FASEC; 2.
PROSITE; PS01286; FASEC; 2.
PROSITE; PS01286; FASEC; 2.
PROSITE; PS010202; FASEC; 2.
PROSITE; PS00022; FASEC; 3; 2.
PROSITE; PS00060; MAM; 2; 1.
Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 931;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             809 813 Missing (in isoform A17).

809 830 Missing (in isoform A0).

802 830 Missing (in isoform A0).

803 FTIG=VSP 004342.

804 805 E -> K (IN REF. 1).

931 AA, 104830 MW; 270CBAE69ADA797C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.9%; Score 164.5; DB 1
29.9%; Pred. No. 3.9e-06;
ative 20; Mismatches 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 (POTENTIAL).
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ID NRP1_RAT STANDARD; PRT; 922 AA.

090WJ0;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F5/8 TYPE C 1.
F5/8 TYPE C 2.
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"Neuropilin is a semaphorin III receptor.";

Cell 90:753-762[1997].

Cell 90:753-762[1997].

Cell 90:753-762[1997].

Cell 90:753-762[1997].

Cell 90:753-762[1997].

Cell 90:753-762[1997].

CERTAIN RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS SYSTEM.

SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SERAPHORINS. IT BINDS TO SEMAPHORIN 34, THE PLGF-2 ISOPORM OF PGF, THE VEGF-165

INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS.

INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS.

INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS.

CHORDON OF VEGF-10DUCED ANGIOGENESIS (BY SIMILARITY).

CHORDON OF VEGF-10DUCED ANGIOGENESIS (BY SIMILARITY).

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CHORDON OF VEGF-10DUCED ANGIOGENESIS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the between the Swiss Institute of Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license enterement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
28-FEB-2003 (Rel. 41, Last annotation update)
Neuropilin-1 precursor (Vascular endothelial cell growth factor 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat;
                                                                                                                                                                                                                     STRAIN=Sprague-Dawley;
MEDLINE=97433085; PubMed=9288754;
Kolodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEUROPILIN-1.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL. CYTOPLASMIC (POTENTIAL).
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InterPro; IPR000421; FA58 C.
InterPro; IPR000998; MAM_domain.
Pfam; PF00431; CUB; 2.
Pfam; PF00754; F5_F8 Lype_C; 2.
Pfam; PF00529; MAM; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00042; CB; 2.
SMART; SM00131; FASEC; 2.
SMART; SM00137; MAM, 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01286; FASEC_1; 2.
PROSITE; PS01286; FASEC_2; 2.
PROSITE; PS001286; FASEC_2; 2.
PROSITE; PS00040; MAM 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF016296; AAC53337.1; -.
HSSP; P12259; 1CZT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00020; MAMDOMAIN.
                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor).
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                                                                                                                                                                               50 ITVSTNGSIHSPREPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFV 109
                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                       7; Gaps
                                                                                                                                                                                                                                      110 EV--EBPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNI 162
                                                                                                                                                                                                                                                   88 EVIDGENEGGRIMGKFCGK-IAPSPVVSSGPFLFIKFVSD-YETHGAGFSIRYEI 140
                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
L6-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neuropilin-2 precursor (Vascular endothelial cell growth factor 165
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Sprague-Dawley;
MEDLINE=97433085; PubMed=9288754;
Kolodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J.,
                                                                                                                           8.8%; Score 163.5; DB 1; Length 922;
                                                                                                                                                       Indels
                                                                                                 103082 MW; CC6F82AD098B0F2E CRC64;
                                                                                                                                          Pred. No. 4.7e-06;
                                                                                                                                                       16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000859; CUB domain.
InterPro; IPR000421; FASB C.
InterPro; IPR000998; MAM_domain.
Pfam; PF00431; CUB; 2.
Pfam; PF00754; F5 F8 LYPE C; 2.
Pfam; PF00629; MAM; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF016297; AAC53338.1; -.
                                                                                                                                          36.5%;
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SMART; SM00042; CUB; 2.
                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                   STANDARD;
       424
150
150
261
300
522
                                                                                                 922 AA;
                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                    receptor 2).
                                                                                                                                                     42;
                                                                                                                                                                                                                                                                                                                                  NRP2 RAT
035276;
                                            CARBOHYD
CARBOHYD
                                                                                   CARBOHYD
SEQUENCE
                    DISULFID
                                                                                                                           Query Match
       DISULFID
                                 CARBOHYD
                                                                       CARBOHYD
                                                                                                                                            Local
                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 PHFEIEKHD---CKYDFIEIRDGDSESADLIGKHCGN-IAPPTIISSGSVLYIKFTSD-Y 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 FSSNKEQNGVQDPQHERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFD 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 FSGHKVRS-QQDPPCGGRINSKDAGXITSPGYPQDYPSHQNCEWVVYAPEPNQKIVLNFN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Sprague-Dawley;
Yamada Y., Hirata Y., Nezu J., Shimane M.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.

Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis and endothelial cell growth, stimulating their proliferation and migration and also has effects on the permeability of blood vessels. May function in the formation of the venous and lymphatic vascular systems during embryogenesis, and also in the maintenance of differentiated lymphatic endothelium in adults. Binds and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       035251;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2004 (Rel. 42, Last annotation update)
15-SEP-2005 (Rel. 42, Last annotation update)
16-SEP-2007 (Rel. 42, Last annotation update)
17-SEP-2008 (Rel. 42, Last annotation update)
18-SEP-2009 (Rel. 42, Last annotation update)
18-SEP-2009 (Rel. 42, Last annotation update)
18-SEP-2009 (Rel. 41, Last annotation update)
18-SEP-2009 (Rel. 41, Last annotation update)
18-SEP-2009 (Rel. 41, Last annotation update)
18-SEP-2009 (Rel. 41, Last annotation update)
18-SEP-2009 (Rel. 41, Last annotation update)
18-SEP-2009 (Rel. 41, Last annotation update)
18-SEP-2009 (Rel. 41, Last annotation update)
18-SEP-2009 (Rel. 41, Last annotation update)
18-SEP-2009 (Rel. 41, Last annotation update)
18-SEP-2009 (Rel. 41, Last annotation update)
18-SEP-2009 (Rel. 41, Last annotation update)
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18-SEP-2009 (Rel. 41, Last annotation update)
18-SEP-2009 (Rel. 41, Last annotation update)
18-SEP-2009 (Rel. 41, Last anno
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
SMART; SM00231; FA58C; 2.

SMART; SM00137; MAM; 1.

PROSITE; P501180; CUB; 2.

PROSITE; P501286; FA58C 1; 2.

PROSITE; P501286; FA58C 2; 2.

PROSITE; P50022; FA58C 3; 2.

PROSITE; P550060; MAM 2; 1.

Transmembrane; Glycoprotein; Neurone; Signal; Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.8%; Score 163; DB 1; Length 925;
13.8%; Pred, No. 5.2e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 N-LINKED (GLCNAC. . .) (POT
103896 MW; 3BF62903F644851C CRC64;
                                                                                                                                                                                                                                                                                                                                     NEUROPILIN-2.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
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F5/8 TYPE C 2.
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                                                                                                                                                                                                                                                                                                                                     833
834
825 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 LYRPTWQLLGKAFVFGRKSR------VVDLNLLTEEVRLYSCTPRNFSVSIREE 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 L-KRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCV---PSKVTKKYHEVLQLRPKTGVR 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89
activates VEGFR-3 (Flt4) receptor (By similarity).

-!-SUBCNIT: Homodimer; non-covalent and antiparallel (By similarity).
-!-SUBCELLULAR LOCATION: Secreted (By similarity).
-!-PTM: Undergoes a complex proteolytic maturation which generates a variety of processed secreted forms with increased activity toward VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer linked by disulfide bonds before secretion. The fully processed VEGF-D is composed mostly of two VEGF homology domains (VHDs) bound by non-covalent interactions (By similarity).
-!-SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 GFSIEHRAVKDVSLERSSRSVLERS-----EQQIRAASTLEELLQVAHSEDWK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 LWRCRIKLKSLANVDSRSTSHRSTRPAATFYDTETLKVIDEBWORTOCSPRETCVEVASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.7%; Score 162.5; DB 1; Length 326;
30.0%; Pred. No. 1.5e-06;
tive 23; Mismatches 80; Indels 39; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00141; FLOST; ...
PROSTIE; PS00249; PDGF 1; 1.
ANGIOGENESIE; PS50278; PDGF 2; 1.
Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat;
Cleavage on pair of basic residues; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
VASCULAR ENDOTHELIAL GROWTH FACTOR D.
POTENTIAL.
4 X 16 AA REPEATS OF C-X(10)-C-X-C-X(1,3)-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
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BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 (INCOMPLETE)
                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR004153; CXCXC_repeat.
InterPro; IPR000072; PD_growth_factor.
Pfam; PF00128; CXCXC; 1.
Pfam; PF00341; PDGF; 1.
ProDom; PD001629; PD_growth_factor; 1.
SWART; SM00141; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---PELVPVKIANHTGCKCLPTG 200
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                                                                                                                                                                                                                                                                                                                                            EMBL; AF014827; AAB66557.1; -.
HSSP; P15692; 1VPP.
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Matches 61, Conservative
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326
317
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326 AA;
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PROPEP
DOMAIN
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RESULT 10

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Remeat;
                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEUROPILIN-1.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last Bequence update)
28-FBB-2003 (Rel. 41, Last amnotation update)
Neuropilin-1 precursor (A5 protein).
                      923 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F5/8 TYPE C 1.
F5/8 TYPE C 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
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                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:106206; Nrp.
InterPro; IPR000859; CUB domain.
InterPro; IPR000421; FASE C.
InterPro; IPR000998; MAM Gomain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00431; CUB; 2.
Pfam; PF00754; F5_F8_type_C; 2.
Pfam; PF00629; MAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0020; MAMDOMAIN.
SNART; SM00042; CUB; 2.
SNART; SM00131; FASSC; 2.
SNART; SM00137; MAM; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01280; FESSC; 2.
PROSITE; PS01286; FASSC; 2.
PROSITE; PS00740; FASSC; 2.
PROSITE; PS00740; MAM 1: 1.
PROSITE; PS00040; MAM 2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D50086; BAA08789.1; -.
                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21
923
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856
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923
141
141
265
583
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                                                                                                                                                            NRP1 OR NRP.
                      NRP1 MOUSE
P97333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor
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NRP1_MOUSE
                                            THILLITIIII AMARAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN BANAN
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                                                                                                                                                                                                                                                                                        31 IKIENPGYLISPGYPHSYHPSEKCEMLIQAPEPYQRIIINFNPHFDLEDRD.---CKYDYV 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -: ISOId=035375-6; Sequence=VSP 004347;
-!- TISSUE SPECIFICITY: EXPRESSED IN DEVELOPING CNS, PNS AND IN SOME NONNEURAL TISSUES INCLUDING LIMB BUDS, DEVELOPING BONES, MUSCLES, INTESTINAL EPITHELIUM, KIDNEY, LUNG AND SUBMANDIBULAR GLAND.
-!- DEVELOPMENTAL STAGE: THE EXPRESSION PATTERN IS VERY DYNAMIC AND IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165
AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.
-i- SUBUNIT: NEUROPILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH
NEUROPILIN-1 IN ORDER TO BE A FUNCTIONAL SEMAPHORIN E RECEPTOR.
-i- SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97470888; PubMed-9331348;
Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;
"Neuropilin-2, a novel member of the neuropilin family, is a high
affinity receptor for the semaphorins Sema E and Sema IV but not Sema
                                                                                                                                                                                                                                         7; Gaps
                                                                                                                                                                                                                                                                                                                                                   88 EVIDGENEGGRLMGKFCGK-IAPSPVVSSGPFLFIKFVSD-YETHGAGFSIRYEI 140
                                                                                                                                                                                                                                                                                                                                   110 EV--EEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNI 162
                                                                                                                                                                                                                                                                                                                                                                                                                                        NRP2 MOUSE STANDARD; PRT; 931 AA.
035375; 035373; 035374; 035376; 035377; 035378;
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Neuropilin-2 precursor (Vascular endothelial cell growth factor 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                               8.6%; Score 160.5; DB 1; Length 923; 36.5%; Pred. No. 8.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS A0; A17; A22; A5; B0 AND B5).
                                                                                                                                                                                                                                         16; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=6;
                                                                                                    N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                     BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=035375-4; Sequence=VSP_004343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=035375-5; Sequence=VSP_004346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=035375-2; Sequence=VSP_004344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sold=035375-3; Sequence=VSP_004345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=035375-1; Sequence=Displayed;
                                          PROBABLE.
           PROBABLE.
                           PROBABLE
                                                        PROBABLE
                                                                                                                                                                                                                                         42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neuron 19:547-559 (1997)
811
2228
2228
2228
2228
3201
251
842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                              522
842
923 AA;
                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=A22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=A17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name≃B5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=A0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=A5;
           DISULPID
                                                                                                                                                 CARBOHYD
                                           DISULPID
                                                        DISULFID
                                                                        DISULFID
                                                                                     DISULFID
                                                                                                     CARBOHYD
                                                                                                                    CARBOHYD
                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSGKEKSWLYTLDPILITIIAMSSLGVLLGATCAGLLLYCT
CSYSGLSSRESCTTLENYNPELYDELAHKYKINHQKCCSBA
-> GTLPPGTEPTVDTVPVPIPAWYYWAAGGAVLVLAS
VVLALVLHYHRPRYAAKKTDHSITYKTSHYNWGAPLAVDEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDFKVDIPETHGGEGYEDEIDDEY EGDWSNSSSSTSGAGDP
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BY SIMILARITY.
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BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
''TINKED (GLCNAC. ..) (POTENTIAL).
''TINKED (GLCNAC. ..) (POTENTIAL).
''TINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane, Glycoprotein, Neurone, Signal, Repeat, Receptor, Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTIKLEQERGSHC (in isoform B0).
/FTId=VSP_004346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEUROPILIN-2.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /frid=VSP 004343.
Missing (In isoform A0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (in isoform A5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
DEVELOPMENTALLY REGULATED.
SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
SIMILARITY: Contains 2 CUB domains.
SIMILARITY: Contains 2 F5/8 type C domains.
SIMILARITY: Contains 1 MAM domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        004345.
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F5/8 TYPE C 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Missing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CUB
                                                                                                                                                                                    EMBL, AF022856, AAC53379.1, -.
EMBL, AF022854, AAC53377.1, -.
EMBL, AF022857, AAC53378.1, -.
EMBL, AF022857, AAC53380.1, -.
EMBL, AF022861, AAC53381.1, -.
                                                                                                                                                                                                                                                                                          InterPro; IPR000859; CUB domain.
InterPro; IPR000421; FA58 C.
InterPro; IPR000598; MAM domain.
Pfam; PF00431; CUB; 2.
Pfam; PF00754; F5 F8 type C; 2.
Pfam; PF00629; MAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS0137; MAM; 1.
PROSITE; PS01280; CUB; 2.
PROSITE; PS01285; FA58C_1; 2.
PROSITE; PS501286; FA58C_2; 2.
PROSITE; PS50022; FA58C_3; 2.
PROSITE; PS50060; MAM 2; 1.
                                                                                                                                                                                                                                                                                                                                                                            PR00020; MAMDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00020; MANDOMAIN
SMART; SM00042; CUB; 2.
SMART; SM00231; FA58C; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                830
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                                                                                                                                                                                                                                                                                   Nrp2
                                                                                                                                                                                                                                                       AF022861; AAC
P12259; 1CZT
                                                                                                                                                                                                                                                                                MGI:1100492;
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                                                                                                                                                                                                                                                                                                                                      61 PRFPHTYPRNIVLVWRLVAVBENVWIQLIFDERFGLEDPEDDICKYDFVEVE--EPSDGT 118
                                                                                                                                                                                                                                                             1 MSLFGLLLVTSALAGQRRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
                                                                                                                                                                                                                                                                                                FUNCTION, AND TISSUE SPECIFICITY.

**MEDLINES-99307076; PUDMEd=1037503;
CORNORS S.A., Trout J., **Ex17503;

"The role of tolloid/mini fin in dorsoventral pattern formation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Development 126:3119-3130(1999).
-!- FUNCTION: Required for patterning ventral tissues of the tail. May increase bone morphogenetic protein (BMP) activity at the end of gastrulation by proteolytic cleavage of chordin and release of BMP
                 EKSMLYTLDPILITIIAMSSLGVLLGATCAGLLLYCTCSYS
GLSSRSCTTLENYNFELYDGLKHKVKINHQKCCSEA -> G
GTLPPGTEPTVDTVPVQPIPAYWYYWAAGGAVLVLASVVL
                                                                   ALVLHYHRERYAAKKTDHSITYKTSHYTNGAPLAVEPTLTI
KLEQERGHUC (in isoform B5).
KTHG=VSP 004347.
786 (FTHG=VSP 004347.
104558 MW; 76F2443F411D2F63 CRC64;
VDIPETHGGEGYEDEIDDEYEGDWSNSSSSTSGAGDPSSGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             closing blastopore with greater expression ventrally. At the animal pole, expressed in the ectoderm flanking the anterior neural plate. At the 10-somite expressed in the developing tailbud and cranial neural crest. At the 20-somite stage, also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygili, Neopterygili, Teleosteli, Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from inactive complexes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blader P., Rastegar S., Fischer N., Straehle U.; "Cleavage of the BMP-4 antagonist chordin by zebrafish Tolloid."; Science 278:1937-1940(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-00T-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Dorsal-ventral patterning tolloid protein precursor (EC 3.4.24.-)
                                                                                                                                                                                   8.6%; Score 160.5; DB 1; Length 931;
10.5%; Pred. No. 8.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                     100 LLGKHCGN-IAPPIIISSGSVLYIKFTSD-YARQGAGFSLRYEI 141
                                                                                                                                                                                                                                                                                                                                                                                                               119 ILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNI 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1022 AA.
                                                                                                                                                                                                                           50; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98057457; PubMed=9395394;
                                                                                                                                                                                                       30.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Mini fin protein).
TOLLOID OR TLD OR MFN.
                                                                                                                                                                                                         est Local Similarity
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   814
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                                                                                                                                CONFLICT
   VARSPLIC
                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                         Matches
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TLD_BRARE
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS, PRO0480; ASTACIN.
SMART; SM00042; CUB; 5.
SMART; SM00042; CUB; 5.
SMART; SM00179; EGP CA; 2.
SMART; SM00179; EGP CA; 2.
SMART; SM00179; EGP CA; 2.
PROSITE; PS010180; CUB; 5.
PROSITE; PS01186; EGF Z; 2.
PROSITE; PS01186; EGF Z; 2.
PROSITE; PS01187; EGF Z; 2.
PROSITE; PS01140; EGF Z; 2.
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N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
SS N-LINKED (GLCNAC. . ) (POTENTIAL).
115536 MW; A68CAIDOE41793F9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CUB 2.
RGF-LIKE 1, CALCIUM-BINDING
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                                                                                                                                                                                                                                                                                              ZFIN, ZDB-GENE-990415-265; tolloid.
InterPro; IPR001506; Astacin.
InterPro; IPR001506; Ast Mydroxyl.
InterPro; IPR0018015; Ast Mydroxyl.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR006209; EGF_IA.
InterPro; IPR006209; EGF_IA.
InterPro; IPR006205; Zn_MTpeptdse.
Pfam; PF01400; Astacin; I.
Pfam; PF01401; GUB; S.
Pfam; PF00009; EGF; Z.
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                                                                                                                                                                                                           EMBL; AF027596; AAC60304.1; -. HSSP; P35555; 1EMN.
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156
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595
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            SOLUTION TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE
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Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;

Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;

"Neuropilin-2 and neuropilin-1 are receptors for the 165-amino acid
form of vascular endothelial growth factor (VEGF) and of placenta

growth factor-2, but only neuropilin-2 functions as a receptor for
the 145-amino acid form of VEGF."

J. Biol. Chem. 275:18040-18045(2000)

C. !- FUNCTION: The membrane-bound isoform 1 is a receptor involved in
the development of the cardiovascular system, in anglogenesis, in
the development of fer in the cardiovascular system, in anglogenesis, in
the development of semaphorins. It binds to semaphorin 3A, The PLGF-2
isoform of semaphorins. It binds to semaphorin 3A, The PLGF-2
isoform of PGF, The VEGF-165 isoform of VEGF and VEGF-16.
Coexpression with KDR results in increased VEGF-165 binding to KDR
as well as increased chemotaxis. It may regulate VEGF-induced
                                            9
                                                                                                              55 NGSIHSPREPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUB-Prostatic adenocarcinoma;
MEDLINE-20183929; PubMed-10688880;
Gagnon M.L., Bielenberg D.R., Gechtman Z., Miao H.-Q., Takashima S., Soker S., Klagsbrun M.; Undensification of a natural soluble neuropilin-1 that binds vascular endothelial growth factor: In vivo expression and antitumor
                                              8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Soker S., Takashima S., Miao H.-O., Neufeld G., Klagsbrun M.; "Neuropilin-1 is expressed by endothelial and tumor cells as an isoform-specific receptor for vascular endothelial growth factor."; Cell 92:735-745(1998).
                                                                                                                                                                                                                                                                                                                                 NRP1 HUMAN STANDARD; PRT; 923 AA.
014786; 060461;
30-MAY-2000 (Rel. 39, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SPP-2003 (Rel. 42, Last annotation update)
Neuropilin-1 precursor (Vascular endothelial cell growth factor 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       angiogenesis.
FUNCTION: The soluble isoform 2 binds VEGF-165 and appears to inhibit its binding to cells. It may also induce apoptosis by sequestering VEGF-165. May bind as well various members of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Neuropilin is a receptor for the axonal chemorepellent semaphorin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                           114 -PSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHY 160
                                                                                                                                                                                                     Length 1022;
Query Match
8.6%; Score 159; DB 1; Length 102
Best Local Similarity 39.8%; Pred. No. 1.3e-05;
Matches 43; Conservative 19; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 22-39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 2), AND SEQUENCE OF 22-31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activity.";
Proc. Natl. Acad. Sci. U.S.A. 97:2573-2578(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20309748; PubMed=10748121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=97433084; PubMed=9288753;
He Z., Tessier-Lavigne M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98188099; PubMed=9529250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NRP1 OR NRP OR VEGF165R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell 90:739-751(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IISSUE=Breast;
                                                                                                                                                                                                                                                                                              RESULT 13
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MIM, 00000501; F. vascular endothelial growth factor receptor. . .; TAS.

RGJ, GO:0005021; F. vascular endothelial growth factor receptor. . .; TAS.

RGJ, GO:0007397; P. Histogenesis and organogenesis; TAS.

RGJ, GO:0007397; P. Histogenesis and organogenesis; TAS.

RGJ, GO:0007397; P. Histogenesis and organogenesis; TAS.

RGJ, GO:0007165; P. Pignaling TAS.

RGJ, GO:0007165; P. Pignaling TAS.

RGJ, GO:0007165; P. Pignaling TAS.

RGJ, GO:0007165; P. RASB.

RGJ, RGJ, RRO00421; RASB.

READ: PRO00421; RASB.

READ: PRO0020; MAMDOMAIN.

RARRT; SMO0021; MAMDOMAIN.

RARRT; SMO0021; MAMJ 1.

RROSITE; PS01180; CUB; 2.

RROSITE; PS01180; CUB; 2.

RROSITE; PS01180; CUB; 2.

RROSITE; PS01180; CUB; 2.

RROSITE; PS01026; FA58C.2; 2.

RROSITE; PS01026; MAMJ 1.

RROSITE; PS01026; MAMJ 1.

RROSITE; PS01026; MAMJ 1.

RROSITE; PS01026; MAMJ 1.

RROSITE; PS01026; MAMJ 1.

RROSITE; PS01026; MAMJ 1.

RROSITE; PS01026; MAMJ 1.

RROSITE; PS01026; MAMJ 1.

RROSITE; PS01026; MAMJ 1.

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RROSITE; PS01026; MAMJ 1.

RROSITE; PS01026; MAMJ 1.

RROSITE; PS01026; MAMJ 1.

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RROSITE; PS01026; MAMJ 1.

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RROSITE; PS01026; MAMJ 1.

RROSITE; PS01026; MAMJ 1.

RROSITE; PS01026; MAMJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the SWISL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions a long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                  semaphorin family. Its expression has an averse effect on blood
vessel number and integrity.
-!- SUBCELLULAR LOCATION: Type I membrane protein. Isoform 2 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor; Alternative splicing; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F5/8 TYPE C 1.
F5/8 TYPE C 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEUROPILIN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AF018956; AAC51759.1; -.
EMBL, AF016060; AAC12921.1; -.
EMBL, AF145712; AF44344.1; -.
PDB; IKEX; 28-JAN-03.
                                                                                    -!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew; HGNC:8004; NRP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
TRANSMEM
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DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 ITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 IKIESPGYLTSPGYPHSYHPSEKCEWLIQAPDPYQRIMINFNPHFDLEDRD---CKYDYV 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                developing chick nervous system.";
Dev. Biol. 170:207-222(1995).
-!- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE
CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF
CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS
SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS (BY
SIMILARITY). SEEMS TO HAVE CALCIUM-INDEPENDENT CELL ADHESION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=White leghorn, TISSUE=Embryonic brain;
MEDLINE=95324761; PubMed=7601310;
Takagi S., Kasuya Y., Shimizu M., Matsuura T., Tsuboi M., Kawakami A.,
Fujisawa H.,
"Expression of a cell adhesion molecule, neuropilin, in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata, Euteleostomi;
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 EV--EEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNI 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 EVEDGENENGHFRGKFCGK-IAPPPVVSSGPFLFIKFVSD-YETHGAGFSIRYEI 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O.F
                                                                                                  | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 
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-!- SUBCEALULAR LOCATION: Type I membrane protein.

-!- SUBCEALULAR LOCATION: Type I membrane protein.

-!- TISSUE SPECIFICITY: DEVELOPING NERVOUS SYSTEM; OPTIC TECTUM
(LAYERS D AND E OF SGFS), AMACRINE CELLS OF RETINA, NEURITES OF
DORSAL ROOT GANGLIA. ALSO EXPRESSED IN NONNEURONAL CELLS, E.G.
BLOOD VESSELS IN THE ENTIRE ENBRRYO.

-!- SIMILARITY: Contains 2 CUB domains.

-!- SIMILARITY: Contains 2 CUB domains.

-!- SIMILARITY: Contains 1 MAM domain.
                                                                                                                                  (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.5%; Score 158.5; DB 1; Length 923; 35.7%; Pred. No. 1.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuropilin-1 precursor (A5 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Mismatches
                                                    BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
173
228
228
424
424
150
150
300
522
842
644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NRP1 OR NRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NRP1 CHICK
P79795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41;
                       DISULFID
DISULFID
DISULFID
                                                                                                           CARBOHYD
                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
  DISULFID
                                                                                                                                                                                                                                                                                                     VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
NRP1_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
     셤
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 ITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLFFDERFGLEDPEDDICKYDFV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 EV--EEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVM--P 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 Q----FTEAVSPSVLP--PSALPLDL-----LINAITAFSTLEDLIRYLEPE 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 ECSRNFTSSSGMIKSPGFPEKYPNSLECTYIIFAPKMSEIILEFESFE-----LEPD 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCOI HUMAN STANDARD; PRT; 449 AA.

(15113; Old-550;
30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Procollagen C-proteinase enhancer protein precursor (PCPE) (Type I procollagen COM+terminal proteinase enhancer) (Type I procollagen COM+terminal proteinase enhancer protein).
institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68; Indels 30; Gaps
                                                                                                                                                                                                                                                                                                                          Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor; Cell adhesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 157; DB 1; Length 914; Pred. No. 1.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
BY SIMILARITY.
1; DD2EE6D6F0CBB68C CRC64;
                                                                                                                                                                                                                                                                                                                                                                      NEUROPILIN-1.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE C 1.
TYPE C 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROBABLE.
PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROBABLE.
PROBABLE.
                                                                                     HSS; P12259; ICZT.
InterPo: IPR000859; CUB_domain.
InterPro: IPR000421; PA58 C.
InterPro: IPR000998; MAM_domain.
PEan; PF00431; CUB; 2.
Pfam; PF00159; MAM, IT.
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                                                                                                                                                                                                           SWART; SM00231; FAA8C; 2.
SWART; SM00231; FAA8C; 2.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01285; FAS6C_1; 2.
PROSITE; PS01286; FAS8C_2; 2.
PROSITE; PS00225; FAS8C_3; 2.
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                                                                     EMBL; D45416; BAA08256.1; -.
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914 AA;
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Matches 52; Conserv
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MEDLINE=22388257; PubMed=12477932;
A TISSUE=HEARIA;
A TRAURE=22388257; PubMed=12477932;
A Rausener R.D., Collins F.S., Wagner L., Schemen C.R., Schuler G.D.,
A Altschul S.F., Zeeberg B., Bettow K.H., Schemen C.F., Bhat N.K.,
A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong E.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Stapleton M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Rha S.S., Loquellano N.A., Peters G.J., Abzmason R.D., Mullahy S.J.,
B Rownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Rha S.S., Loquellano N.A., Peters G.J., Maraket J.A., Gabarane P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,
A Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
B Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
B Hakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
B Nuterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
Chentrion and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                             "Type I procollagen COOH-terminal processes community of the identification, primary structure, and chromosomal localization of the cognate human gene (PCOLCE).";
J. Biol. Chem. 269:26280-26285(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hirahara I., Syoufuda K., Harada K., Tomita M., Urakami K., Terai H., Morisaki N., Saito Y.; "Smooth muscle cell derived procollagen C-protease enhancer protein."; Cell Struct. Funct. 21:662-662(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Large-scale sequencing of two regions in human chromosome 7q22: analysis of 650 kb of genomic sequence around the BPO and CUTL1 loci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mott J.D., Thomas C.L., Rosenbach M.T., Takahara K., Greenspan D.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-99134301, PubMed-9933570;
Scott I.C., Clark T.G., TakAbara K., Hoffman G.G., Greenspan D.S.;
"Structural organization and expression patterns of the human and
mouse genes for the type I procollagen COOH-terminal proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-99018118; PubMed=9799793;
Gloeckner G., Scherer S., Schattevoy R., Boright A.P., Weber J.,
Tsui L.-C., Rosenthal A.;
                                                                                                                                                                                                              Takahara K., Kessler E., Binlaminov L., Brusel M., Eddy R.L., Jani-Sait S., Shows T.B., Greenspan D.S.; "Type I procollagen COOH-terminal proteinase enhancer protein:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PARTIAL SEQUENCE, AND CHARACTERIZATION OF INHIBITORY ACTIVITY.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished observations (FEB-2000).
                                                                                                                                                      IISSUE=Placenta;
MEDLINE=95014462; PubMed=7523404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=10625689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Res. 8:1060-1073(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REVISIONS TO 56; 154 AND 373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enhancer protein.";
Genomics 55:229-234(1999),
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                                           WCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 GSIHSPREPHT-YPRNTVLVWRLVAVEENVWIQLIFDERFGLEDPEDDICKYDFVEV--- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 EEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFT--- 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                224 AVSDDSRRLGKFCGD-AVPGSISSEGNELLVQFVSDLSVTAD-GFSASYK-TLFRGTAKE 280
-i- FUNCTION: BINDS TO THE COCH-TERMINAL PROPERTIDE OF TYPE I
PROCOLLAGEN AND ENHANCES PROCOLLAGEN C-PROTEINASE ACTIVITY.
-i- FUNCTION: C-TERMINAL PROCESSED PART OF PCPE (CT-PCPE) MAY HAVE AN METALLOPROTEINASE INHIBITORY ACTIVITY.
-i- SUBCELLULAR LOCATION: Secreted.
-i- FINI. C-TERMINALLY PROCESSED AT MULTIPLE POSITIONS.
-i- SIMILARITY: Contains 1 UTR domain.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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GO; GO:0008151; P:cell growth and/or maintenance; TAS.
GO; GO:0007275; P:development; TAS.
GO:0007275; P:development; TAS.
InterPro; IPR000859; CUB domain.
InterPro; IPR001134; Netrin_C.
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33.8%; Pred. No. 1.2e-05;
tive 22; Mismatches 50;
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EMBL, AR003549; BAA32811; --
EMBL, AF063365; AAC78800.1; --
EMBL; BC00574; AAD16041.1; --
EMBL; BC00574; AAH00574.1; --
EMBL; BC03205; AAH33205.1; --
GENEW; HGNK:8738; PCOLCE.
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Pfam; PF00431; CUB; 2.
SMART; SM00643; C345C; 1.
SMART; SM00042; CUB; 2.
GLYCOPICTE; PS01180; CUB; 2.
SIGNAL
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Search completed: November 25, 2003, 21:02:50 Job time : 8.55655 secs

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(without alignments)
2922.663 Million cell updates/sec
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1 MSLFGLLLVTSALAGQRRGT......DVALEHHEECDCVCRGSTGG 345
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_rvirus:\*
sp\_bacteriap:\*
sp\_archeap:\*

## SUMMARIES

Description	Q9nral homo sapien	Q9u122 homo sapien	Q9qy71 mus musculu	Q8ci19 mus musculu	Q9eqx6 rattus norv	09jhv8 mus musculu	Q9i946 gallus gall	Q8k429 rattus norv	Q9gzp0 homo sapien	Q9bwv5 homo sapien	Q925i7 mus musculu	Q9eqt1 rattus norv	Q8k213 mus musculu	Q8qfx6 brachydanio	Q8axp1 brachydanio	O60494 homo sapien
ID	Q9NRA1	Q9UL22	Q9QY71	Q8CI19	OPEQX6	8VHC6Q	091946	Q8K429	Q9GZP0	Q9BWV5	092517	Q9EQT1	Q8K2L3	Q8QFX6	Q8AXP1	060494
DB	4	4	Ħ	11	11	11	13	11	4	4	11	Ħ	11	13	13	4
Query Match Length DB	345	345	345	345	345	345	345	258	370	364	370	370	261	923	923	3623
Query Match	100.0	93.6	89.6	89.5	88.6	88.0	86.9	67.8	39.9	39.9	39.7	39.6	23.4	10.3	10.3	9.8
Score	1858	1851	1664	1662	1646	1635	1614	1260	741.5	740.5	737.5	736	435.5	190.5	190.5	183
Result No.		8	m	4	'n	9	,	σ	6	10	11	12	13	14	15	16

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13 057658	11 Q99JM4	13 Q91925	11 070244	11 Q9WVM6	13 057381	4 Q9UQ00	4 Q9Y6L7	11 092135	11 Q8BPZ0	11 Q8QZY7	4 Q9H2E2	4 Q9H2E4	4 Q9H2D5	4 Q9H2D4	4 Q9H2E3	11 Q9QX38	6 Q9TU53	13 Q8JI28	4 Q96190	4 Q96IH5	4 Q9H2E1	13 QBUVR0	13 Q8UVQ9	13 Q9DER7	4 Q9UKZ9	13 057382	11 Q91ZE4	4 Q9BRH3
691	34	977	3623	1012	735	926	1015	241	145	926	555	901	901	906	906	921	3620	1007	609	644	704	919	936	1008	415	1019	326	276
9.6	9.7	9,5	و. ت	9.3	6.5	6	9.5	6.6	6.8	8.9	6.8	8.9	6.8	8.9	6.8	8.8	8.8	8.7	8.5	8.5	8.5	8.5	8 .u	8.4	8.2	8.3	8.2	8.1
182	180	176	176	172	171	171	171	169	165.5	165.5	164.5	164.5	164.5	164.5	164.5	163.5	163.5	161.5	158.5	158.5	158.5	157.5	157.5	157	153	153	151.5	151
17	18	18	20	7	20	10	4.0	2.5	26	27	8	53	30	31	35	33	34	35	36	37	38	39	40	4.1	42	43	44	45

## ALIGNMENTS

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Gaps
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TISSUB-Lung;

MEDLINE=2026201; PubMed=10806482;

MEDLINE=2026201; PubMed=10806482;

Li X., Ponten A., Aase K., Karlsson L., Abramsson A., Uutela M.,

Backstrom G., Hellstrom M., Bostrom H., Li H., Soriano P.,

Backstoltz C., Heldin C.-H., Alitalo K., Ostman A., Eriksson U.;

PDGF-C is a new protease-activated ligand for the PDGF alphareceptor.";

I ar. Cell Balol. 2:302-309(2000).

I Nat. Cell Balol. 2:302-309(2000).

I SHBL; AF244813; AAF80557.1;

IL SIMILARITY: CONTAINS I CUB DOWAIN.

REBL; AF244813; AAF805597.1;

RICEPPO; IPRO00692; CUB domain.

RICEPPO; IPRO00692; CUB domain.

REAM: PF00411; CUB; 1.

RARRI; SM0044; CUB; 1.
                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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PROSITE; PS50278; PDGF 2; 1.
SEQUENCE 345 AA; 39043 MW; 590889CEA55CC5EA CRC64;
                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
blatelet-derived growth factor C.
                              345 AA.
                            PRT;
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Matches 345; Conservative
                               PRELIMINARY;
                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                    PREPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVERPSDGTIL 120
                                                                                                           121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA 180
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           1 MSLPGLLLVTSALAGQRRGTQAESNLSSKPQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
MEDLINE=20317014; PubMed=10858496;
Hamada T., Ui-Tei K., Miyata Y.;
Hamada T., Ui-Tei K., Miyata Y.;
Ha novel gene derived from developing spinal cords, SCDGF, is a unique member of the PDGF/VEGF family.";
PEBS Lett. 475:97-102(2000).
1 MSLFGLLLVTSALAGORRGTQAESNLSSKFOFSSNKEQNGVQDPQHERIITVSTNGSIHS
                                                                                                                                                                  LPLDLINNAITAFSTLEDLIRYLEPERWOLDLEDLYRPTWOLLGKAFVFGRKSRVVDLNL
                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Secretory growth factor-like protein FALLOTEIN (SPINAL CORD-derived HSCDGF OR PDGFC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tsal Y.J., Lee R.K.K., Lin S.P.; "Fallotein, a novel growth factor like gene identified in human
                                                                                                                                                                                                                                                                              301 VIKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345
                                                                                                                                                                                                                                                                                             VIKKYHEVLQLRPKTGVRGLHKSLIDVALEHHERCDCVCRGSTGG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
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Gao Z., Hart C., Piddington C., Sheppard P., Shoemaker K.,
Gilbertson D., West J., O'Hara P.J.;
"Platelet-derived growth factor C (PDGF-C), a novel growth factor that
binds to PDGF alpha receptor.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                   1 MSLFGLLLVTSALAGQRRGTQAESNLSSKFQFSSNKFQNGVQDPQHERIITVSTNGSIHS
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Tsai Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;
Tendra cloning of fallotein from mouse ovary.";
Submitted (JAN-1999), to the EMBL/GenBank/DDBJ databases.
                                                                                                                                         99.6%; Score 1851; DB 4; Length 345; 99.4%; Pred. No. 1.9e-171; tive 2; Mismatches 0; Indels (
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PROSITE; PS01180; CUB; 1.
PROSITE; PS50278; PDGF 2; 1.
SEQUENCE 345 AA; 39029 MW; CDE9E51F40633E78 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Matches 343; Conservative
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                                                                                                                                                        Query Match
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PREPHTYPRNIVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTIL 120
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      GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA 180
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                                  LPLDLINNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL
                                                                                                                      Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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STRAIN=Wister; TISSUE=Kidney;
MEDLINE=21092670; PubMed=11162582;
MEDLINE=21092670; PubMed=11162582;
MEDLINE=21092670; PubMed=11162582;
MADLecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to SCDGF/POBC-C/fallotein.";
EDGEF/POBC-C/fallotein.";
EDGEF
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                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Spinal cord-derived growth factor.
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Matches 295; Conservative
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Q9EQX6,
01-MAR-2001
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Wusaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NGBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                   Query Match

Best Local Similarity 86.7%; Pred. No. 3e-153;
Matches 299; Conservative 28; Mismatches 18; Indels 0,
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EMBL; AK042767; BAC31358.1; -.
EMBL; AK052947; BAC35216.1; -.
EMBL; AK052947; BAC35216.1; -.
EMBL; AK052947; BAC35216.1; -.
EMBL; AK052947; BAC35216.1; -.
EMBL; AK0500859; CUB domain.
InterPro; IPR000072; PD_Growth_factor.
FEm; PF00431; PDGF; 1.
SMART; SM00042; CUB; 1.
SMART; SM0141; PDGF; 1.
PROSITE; PS0188; PDGF; 2; 1.
PROSITE; PS0278; PDGF 2; 1.
SEQUENCE 345 AA; 38741 MW; 3AS8A1F701B84EA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BC037696; AAH37696.1; -
SEQUENCE 345 AA: 38741 MW; 9ASBAOSCGCOE9614 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Platelet-derived growth factor, C polypeptide.
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Best Local Similarity 86.4%
Matches 298; Conservative
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STRAIN=CZECH II;
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121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PKFPHTYPRNITVLVWRLVAVDENVWIQLTFDERFGLEDPBDDICKYDFVEVEFERDGTVL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAINS—White leghorn; TISSUE-Spinal cord;
MEDLINE=20317014; PubMed=10858496;
MEDLINE=20317014; PubMed=10858496;
Hamada T., Ui-Tei K., Miyata Y.;
Hamada T., Ui-Tei K., Miyata Y.;
Hamada T., Ui-Tei K., Miyata Y.;
Hamada T., Ui-Tei K., Miyata Y.;
Hamada T., Ui-Tei K., Miyata Y.;
Hamada T., Ui-Tei K., Miyata Y.;
Hamada T., Ui-Tei K., Miyata Y.;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                           ылыы улышы (слискел).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.9%; Score 1614; DB 13; Length 345; 83.8%; Pred. No. 2.2e-148; ive 31; Mismatches 25; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 345 AA; 38940 MW; 97ACEA992BF5128C CRC64;
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                     Last sequence update)
Last annotation update)
  Created)
01-OCT-2000 (TrEMBLrel. 15, Create 01-OCT-2000 (TrEMBLrel. 15, Last 8 01-MAR-2003 (TrEMBLrel. 23, Last 8 Spinal cord-derived growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00431; CUB; 1.
Pfam; PF00341; PDGF; 1.
SMART; SM00141; PDGF; 1.
SMART; SM00141; PDGF; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01278; PDGF_2; SEQUENCE 345 AA; 38940
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Best Local Similarity
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                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                  Gallus.
NCBI_TaxID=9031;
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       LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK 300
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MEDLINE-20417814; PubMed=10960785;
Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;
The mouse Pdgfc gene: dynamic expression in embryonic tissues during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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Best Local Similarity 85.5%; Pred. No. 2e-150;
Matches 295; Conservative 28; Mismatches 22;
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wech. Dev. 96:209-213 (2000).

-! SIMILARITY: CONTAINS 1 CUB DOMAIN.
EMBL, AF266725; AAF91483.1; -.
MGD; MGI: 1885631; FGGfc.
InterPro; IPR000059; CUB, domain.
InterPro; IPR000072; PD_Growth_factor.
Pfam; PR00431; CUB; 1.
SMART; SM00141; PDGF; 1.
PROSITE; FS01180; CUB; 1.
PROSITE; PS01180; CUB; 1.
SROSITE; PS01180; CUB; 1.
SROSITE; PS01180; CUB; 1.
SROURCE 345 AA; 38886 MW; FA1486BED
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01-007-2000 (TrEMBLrel. 15, Last
01-MAR-2003 (TrEMBLrel. 23, Last
platelet-derived growth factor C.
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PRELIMINARY;
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Best Local Similarity
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                                               SEQUENCE FROM N.A. PubMed=11331881;
 Wistow G.;
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Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S.,
Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,
Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q.,
Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.;
Submitted (DEC-1998) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
spinal CORD-4 derived growth factor-B (MSTP036) (IRIS-expressed growth factor long form) (Platelet-derived growth factor D).
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hamada T., Ui-Tei K., Imaki J., Miyata Y.,;
"Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to
SCDGF/PDGF-C/fallotein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                   ö
STRAIN=Sprague-Dawley, TISSUE=Skin;
Brown S.A., Coberly D.M., Rohrich R.R., Chao J.J.;
"Platelet Derived Growth Factor C (PDGF-C) Expression in Wound
                                                                                                                                                                                                                        Length 258;
                                                                                                                                                                                                                                                   12; Indels
                                        258 258 AA; 29255 MW; 88625B989FCC3F8B CRC64;
                                                                                                                                                                                                                        67.8%; Score 1260; DB 11;
85.6%; Pred. No. 3.9e-114;
iive 25; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  370 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 GNCACCLHNCNECQCVP 257
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                                                                                                                                                                                                                                         Best Local Similarity 85.6
Matches 220; Conservative
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TISSUE=Iris;
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NON TER
SEQUENCE
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A MEDLINE=21231380; PubMed=11331882;

A MEDLINE=21231380; PubMed=11331882;

LaRochelle W.J., Jeffers M., McDonald W.F., Chillakuru R.A.,

A Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,

Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shimkets J.,

Burgess C.E., Rothberg J.M., Lichenstein H.S.;

R. Cell Biol. 3:517-521(2001).

R. Cell Biol. 3:517-521(2001).

R. Cell Biol. 3:517-521(2001).

R. MBL; AR033832; BAB18903.1; -.

BRBL; AR13346; AAK38840.1; -.

BRBL; AR35584; AAK38840.1; -.

BRBL; AR35584; AAK38840.1; -.

BRBL; AR35584; AAK38840.1; -.

BRBL; AR35584; AAK38840.1; -.

BRBL; AR3584; AR38840.1; -.

BRBL; AR38840.00072; DG_Gowdin.

BRBL; AR00042; CUB. 1..

BR SWART; SMO0441; CUB; 1..

BR SWART; SMO0441; CUB; 1..

BR PROSITE; PSG0130; TONB_DEPENDENT_REC_1; 1.

BR ROSITE; PSG0130; TONB_DEPENDENT_REC_1; 1.

BR ROSITE; PSG0130; TONB_DEPENDENT_REC_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 --ILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSBPGFCIHYNIVMPQFTEAV---- 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTWQLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLV 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRP---KTGVRGLHKSLTDVALEHHEB 334
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                                                                                                                        Bergsten B., Uutela M., Li X., Pietras K., Ostman A., Heldin C.H., Alitalo K., Eriksson U.; Poge-Dis a specific, protease-activated ligand for the PDGF beta-receptor.";
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"Iris-expressed Growth Factor (IEGF).";
Submitted (FBB-2001) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GNCGCGTVNWRSCTCNSGKTVKKXHEVLQFEPGHIKRRGRAKTWALVDIQLDHHERCDCI 357
                                                                                                                                                                                                                                                                                                                                                                                                                               FPHTYPRNIVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVERFSDGT--IL 120
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       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 23, Last annotation update)
1ris-expressed growth factor short form (Spinal cord-derived growth factor-B).
                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                             Query Match

39.9%; Score 740.5; DB 4; Length 364;
Best Local Similarity 43.2%; Pred. No. 2e-63;
Matches 156; Conservative 61; Mismatches 113; Indels 31;
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Strausberg R.;

Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

BMBL, AYO27318; AAR20082.1; -.

R BMBL, BC030645; AAH30645.1; -.

InterPro; IPR000072; PD_Growth.factor.

R InterPro; IPR000073; PD_Growth.factor.

R InterPro; IPR000073; PD_Growth.factor.

R InterPro; IPR000073; TOMB_boxC.

R Pfam; PF00431; CUB; 1.

PROSITE; PS01180; CUB; 1.

PROSITE; PS01380; CUB; 2; 1.

PROSITE; PS00430; TONB_DEPENDENT_REC_1; 1.
                                                                                                                                                         "Iris-expressed Growth Factor (IEGF).";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2003 (TrEMBLrel. 23,
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Best Local Similarity
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Q92517
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SEQUENCE FROM N.A.

STRAIN=CSPIL/6J; TISSUB=Body;
A Arakawa T., Arai A., Aono H.,
A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A Hanagaki T., Hara A., Hayateu N., Hiramoco K., Hiraoka T., Hori F.,
A Imotani K., Ishii Y., Itoh M., Izawa M., Koaukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
A Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
A Sano H., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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STRAIR=CE7BL/G1 TISSUE=Body;
MEDLINE=C57BL/G1 TISSUE=Body;
MEDLINE=C57BL/G409374;
PubMed=11041159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Franci J., Shibata Y., Muramatsu M., Hayashizaki Y.;
Franci J., Shibata J., Shibata K., Itoh M.,
Franci J., Shibata K., Itoh M., Shibata K., Itoh M.,
Genome Res. 10:1617-1630(2000).
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Platelet-derived growth factor D (18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110003109 product:platelet-derived growth factor D).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21231380, PubMed=11331882, LaRochelle W.J., Jeffers M., McDonald W.F., Chillakuru R.A., LaRochelle W.J., Jeffers M., McDonald W.F., Chillakuru R.A., Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shimkets J., Shimkets R.A., Rothberg J.M., Lichenstein H.S.; Novel Protease-Activated Growth Factor."; Nat. Cell Biol. 3:517-521(2001).
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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STRAIN=C57BL/6J; TISSUE=Body;
MEDLINE=99279253; PubMed=10349636;
Carinci P., Hayashizaki Y.;
Carinci P., Hayashizaki Y.;
Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/6J; TISSUE=Body;
MEDLINE=21085660; PubMed=11217851;
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MEDLINE=22354683; PubMed=12466851;
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SMART; SM00042; CUB; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLPPSALPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSR 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
TYEXBI integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
C. - SIMILARIYI CONTAINS 1 CUB DOWAIN.
BMBL; AR335583; AAX38839.1;
R EMBL; AR03359; BAB22735.2; -.
R MD; MG1:1919035; Paggfd.
R InterPro; IPR000085; CUB domain.
R InterPro; IPR000085; CUB domain.
R Pfam; Pr00411; CUB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 ORRGIQAESNLSSKFOFSSNKEQNGVQD-POHERIITVSTNGSIHSPRFPHTYPRNTVLV
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21092670; PubMed=11162582;
MEDLINE-21092670; PubMed=11162582;
MEDLINE-21092670; PubMed=11162582;
MOLOCULAR CLOMING OF SCHOF-B, a Novel Growth Factor Homologous SCHOF-PDGF-C/fallotein.";
Blochem. Blophys. Res. Commun. 280:733-737(2001).
-1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
EMBL; AB052170; BABL8320.1;
InterPro; IPR000859; CUB_domain.
InterPro; IPR000859; CUB_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.7%; Score 737.5; DB 11; Length 370; 44.0%; Pred. No. 4e-63; Live 59; Mismatches 103; Indels 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS01180; CUB; 1.
PROSITE; PS50278; PDGF 2; 1.
SEQUENCE 370 AA; 42809 MW; 9E80B4CF6813BFBE CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Spinal-cord derived growth factor-B.
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SMART; SM00141; PDGF; 1.
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WRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGT--1LGRWCGSGTVPGK 132
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                                                                                                                                                                                                                                                       37 EQNGVQD-PQHERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFG
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Wakaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi;
Mammalla, Eutheria; Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                  28;
                                                                                                                                           Length 370;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to platelet-derived growth factor, D polypeptide.
                                                                                                                                                                                                  Indels
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submitted (UUN-2002) to the EMBL/GenBark/DDBJ databases. 
Submitted (UUN-2002) to the EMBL/GenBark/DDBJ databases. 
EMBL, BC030896; AAH30896.1; -
EMBL, BC030896; AAH30896.1; -
EMBL, BC030896; CUB_domain. 
InterPro; IPR000869; CUB_domain. 
Pfam; PF00431; CUB; 1. 
PROSITE; PS01180; CUB; 1. 
SEQUENCE 261 AA; 30228 MW; ZEEC3F6373A52D09 CRC64;
SMART; SM00141; PDGF; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS50278; PDGF 2; 1.
SEQUENCE 370 AA; 42809 MW; 7BE8A251F679BF73 CRC64;
                                                                                                                                        39.6%; Score 736; DB 11;
45.6%; Pred. No. 5.6e-63;
iive 57; Mismatches 93;
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                                                                                                                                                                                                        Matches 149; Conservative
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157 KSPGFPEKYPNNLDCTFMIPAPKMSEIVLEPESFELEPDTQP-----PAGVFCRYDRL 209
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                                                 RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 WCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMP-----QFTEAVSPSVL 176
                                                              175 VLPPSALPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSR 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                   A Lee P., Goishi K., Davidson A., Mannix R., Zon L., Klagsbrun M.;
Lee P., Goishi K., Davidson A., Mannix R., Zon L., Klagsbrun M.;
"Neuropilin-1 is required for normal vascular development and is a
"Neuropilin-1 is required for normal vascular development and is a
"nediator of VEGF-dependent angiogenesis in zebrafish.";
Submitted (NOV-2001) to the EMBL/GenBank/DbBJ databases.
-!-SUBCELLUIAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
C -!- SIMILARITY: CONTAINS I TES DOMAINS.
C -!- SIMILARITY: CONTAINS 1 WAM DOMAIN.
-!- SIMILARITY: CONTAINS 1 FS/8 TYPE C DOMAIN.
-!- SIMILARITY: CONTAINS 1 FS/8 TYPE C DOMAIN.
-!- SIMILARITY: CONTAINS 1 MAM Gomain.
R InterPro: IPRO00999; MAM Gomain.
R Pfam; PF00421; FA58 C.
R Pfam; PF00429; PS F9 LYPE C; 2.
R Pfam; PF00529; MAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 GLLLVTSALAGQRRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRFP
                                                                                                                                                                                                                                                                                                               Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Meopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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SEQUENCE 923 AA; 102492 MW; 2ED84B129AA92B2D CRC64;
   133 QISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAV---
                                                                                                                                                                                                                                                     Q8GFX6;
01-UNN-2002 (TrEMBLrel. 21, Created)
01-J.NN-2002 (TrEMBLrel. 21, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
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SMART; SM0201; FASEC; 2.
SMART; SM02011; FASEC; 2.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01285; FASEC 1; 1.
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44 VSYYPSQKCIWVITAPGFNQRILINFNFHFDLEDRE---CKYDYVBVRDGVDENQLVGK 100
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shôji W., Tawarayama H.;
"The cloning and expression of neuropilin-1.";
Submitted (UTU-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, ABO87775; BACS3657.1; -.
SEQUENCE 923 AA; 102541 MW; OE6CE33ED28A21F7 CRC64;
                                                                 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
923 AA
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PRT;
PRELIMINARY;
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November 25, 2003, 22:28:25; Search time 3795.28 Seconds (without alignments) 16556.656 Million cell updates/sec
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Pref. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	1 8	AK210624 Sequence AR232022 Sequence	AX047650 Sequence	AX391260 Sequence	OTTO SA	edne	AX739931 Sequence	AF260738 Homo sapi	AR267280 Sequence	AX044518 Sequence	eque	AB033831 Homo sapı BD004757 Novel VEG	ntik	AR282992 Sequence AX027935 Sequence	AF266467 Mus muscu	AR26/281 Sequence AR282985 Sequence	AX044520 Sequence	AF117608 Mus muscu	AB033830 Rattus no	AF286725 Mus muscu	AB033829 Gallus ga	AC092608 Homo Bapi AR282950 Sequence	Sequence	AF508348 Rattus no AX027960 Sequence	AC015451 Homo sapi	AX02/962 Sequence AX027981 Sequence	AX027963 Sequence	AX027970 Sequence	AX027993 Sequence	AX02/968 Sequence AX027989 Sequence	AX027964 Sequence AX027984 Sequence		;	DNA linear PAT 20-JUN-2002			cular endothelial cell growth	ln 1
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Oy 964 ATCACCACCAGCAGCTCTTGCCCA	1084	DD 1261 CTTTTGAGGGGGCCTAAAGGACAGGCCTAAAGGACAAGGACCAAAGGACAAGAACAAGAACAAGAACAAGAACAAGAACAAGAACAAGAACAAC	1541	1601	1661		Db 1781 ACCAGAACATGTGTATGTACTACAACATGTACTACAACATGTACTATGTACTAGGGGGACATGTGTATGTA	Db 1841 TAAACTTGTGTCATGCTGATAGG		2727390	NISM	TITLE Nucleic acids encoding var (VEGF-E) JOURNAL Patent: 105 455283-A 1514	rce	Query Match Query Match Best Local Similarity 99.9%; Pree Matches 1332. Conservative 1: 1	AGTTTTCCAG	
Location/Qu 	\$_\$		124 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAAC 183 	184 TTACGTTTGATGAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGGATT 243 	244 TIGTAGAAGCTGAGGAACCCAGTGATGGAACTATATTAGGGCGCTGGTGTGGTTCTGGTA 303 	304 CTGTACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATG 363 	364 AATATTTTCCTTCTGAACCAGGGTTCTGCATCCACTACAACATTGTAGTGCCACAATTCA 423 701 AATATTTTCCTTCTGAACCAGGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCA 760	424 CAGAAGCIGIGAGICCIICAGIGCIACCCCIITGACIIIGCCACIGGACCIGCIAAIA 483 	484 AIGCIAIDACTGCCITIAGIACCITGGAAGACCITAITCGAIAICTTGAACCAAGAGAG 543 	544 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG 603 	604 TITITGGAAGAAAATCCAGAGTGGATCTGAACCTTCTAACAGAGGTAAGATTAT 663 	664 ACAGCIGCACACCTCGIAACTICTCAGIGICCATAAGGAAAGAACTAAAGAGAACCGAIA 723 	724 CCATTITCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGGAACTGTGCCTGTTGTC 783 	784 TCCACAATTGCAATGACAATGTCCCAAGCAAAGTTACTAAAAATTACCACGAGG 843 	844 TCCTTCAGTTGAGACCAAASACCGGTGTCAGGGGATTGCACAAATCACTCACCGACGTGG 903 	904 CCCTGGAGCACCATGAGGAGTGTGACTGTGTGCAGAGGAGGAGCACAGGAGATAGCCGC 963
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	RESULT 4 AX391260 LOCUGS LOCUGS LOCUGS LOCUGS AX391260 AX391260 DEFINITION Sequence 3 from Patent WO0073445. ACCESSION AX391260.1 GI:19699933 KEYWORDS KEYWORDS Homo sapiens (human) ORGANISM Homo sapiens (human) Mammalia; Butheria; Primates; Catan Mammalia; Butheria; Primates; Catan REFRENCE AUTHORS FETTATA, N. Williams, P.M., Baker, K Godowski, P.J., Gurney, A.L., Kuo, S.: Godowski, P.J., Gurney, A.L., Kuo, S.:	Pitti,R.M., Wood,W.I., Gerber,H., Watanabe,C.K. Frank, Wood,W.I., Gerber,H., Watanabe,C.K.  Frank, Wood,W.I., Gerber,H., Wood,W.I., Gerber,H., Frank, Wood,W.I., Gerber,H., Genentech Inc. (US)  FEATURES  1. 2849    Corganism="Homo sapiens"   Mol.type="genomic DNA"   Mol.t	Duery Ma 3est Loc Matches	224   CAATITATIACTOISICIACITATIAGAMAIATIA   CAAGAAATACGGTCTTGGTATGGAGATTAGTA   CAAGAAATACGGTCTTGGTATGGAGATTAGTA   CAAGAAATACGGTCTTGGTATGGAGATTAGTAGAAATACGGTCTTGGTATGGAGATTAGGAGATTAGGAGAAATACGGTTGAGAAAAAAATATGGAGAAAAAAAA
244 TTGTAGAAGTTGAGGAACCCAGTGATGGAACTATATTAGGGCGCTGGTGTGTTCTGGTA 303 607 TTGTAGAAGTTGAGGAACCCAGTGATGGAACTATATTAGGGCGCTGGTGTGTTCTGGTA 666 304 CTGTACCAGGAAACAGAATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATTGTATCTGTTG 363 667 CTGTACCAGGAAACAGATTTCTTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATG 363 667 CTGTACCAGGAAACAGATTTTTTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATG 364 AATATTTTCCTTCTTGAACCAGGGTTCTGCATCCACTACAATTCA 423 727 AATATTTTCCTTCTTGAACCAGGGTTCTGCATCCACTACACATTGTCATGCCACAATTCA 736 424 CAGAAGCTGTGAGTCCTTCCGCATCCCCTTCAGCTTTGCCACAATTCA 736 727 CAGAAGCTGTGAGTCCTTCCGCTACCCCCTTCAGCTTTGCCACAATTCA 736 727 CAGAAGCTGTGAGTCCTACCCCCTTCAGCTTTGCCATGCCACAATTCA 736 728 CAGAAGCTGTGAGTCCTACCCCCTTCAGCTTTGCCACGACTTGATAATA 483 729 CAGAAGCTGTGAGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAAATA 846	484 ATGCTATAACTGCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGAT 543	ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA CCATTTTCTGGCCCAGGTTGTCTCCTGGTTAAACGCTGGGGGAACTGTGCCTGTTGTC CCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACTGTGCCTGTTGTC CCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACTGTGCCTGTTGTC TCCACAATTGCAATGAATGTCTCCCAAGCAAGTTACTAAAAAATACCACGAGG	1207 TĊĊTTĊĀĞTTĞAĞACĞAAĞAACGGGTGTCAGGGGATTGCACAAATCACTCACCGACGTGG 1266  904 CCCTGGAGCACCATGAGGAGTGTGACTGTGTGCAGGAGGAGGACAGGAGGAGGATGGCGC 963	1387 CGTATGCGTTATCTCCCATCCTTAATCTCTCTCAGGGGCCTTCATCATCTCTCGG 1446  1084 GATTTACAGTGCATTCTCAAAGAGGAGACTCTCAACAGGACCTTTCATCTCTCAG 1446  1084 GATTTACAGTGCATTCTGAAAGAGAGACATCAACAGAATTGGGGACTTGTGCAACACT 1143  1447 GATTTACAGTGCATTCTGAAAGAGACACACAAACAGAATTGGGAACAACACT 1506  1146 CTTTTGAAGAGAGGCCTAAAGGACAACAAACAGAATTACAATCGTGGAAAAAAAA
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ö TGCTTAACTCTAAAGCTCCATGTCCTGGG 1383 TTTTAAAAAGGAACTATGTTGCTATGAAT 1503 ||||||||||||||||||||||||||||| TTTTAAAAAGGAACTATGTTGCTATGAAT 1866 426 486 243 909 999 ATCAAATTAGGATAAGATTTGTATCTGATG 363 linear PAT 23-MAR-2002 123 303 ICCACTACAACATIGICAIGCCACAATICA 423 K.P., Ashkenazi,A.J., Goddard,A., I.S., Mark,M.R., Marsters,S.A., Gerritsen,M.E., Paoni,N.F. and 63 genesis and cardiovascularization 10; niata; Vertebrata; Euteleostomi; arrhini; Hominidae; Homo. CTATATTAGGGCGCTGGTGGTGGTTCTGGTA ITCACAGCCCAAGGTTTCCTCATACTTATC AGAACGGAGTACAAGATCCTCAGCATGAGA Gaps 0; DB 6; Length 2849; 1 others 0; Indels DNA 50 t .6; 0; hes

ANATTHECTICAL CONSIDERATION CONTROLLED TO THE CO	Db         1807         ACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAAT 186           Qy         1504         TAAACTTGTGTCATGCTGATAGGACAGACTGGA 1536           Db         1867         TAAACTTGTGTCATGCTGATAGGACAGACTGGA 1899	AX464152 AX464152 E 2849 bp DNA linear PAT 16-JUL-2002 LOCUS Sequence 285 from Patent W00140466.  ACCESSION AX464152 GI:21899092 ACCESSION AX464152.1 GI:21899092 Homo sapiens (human) ACGANISM Homo sapiens (human) AMAMISM HOMO SAPIENS BULARYORS SOURCE AMAMMALIA; Eutheria; Primates; Catarrhini; Hominidae; Homo.  MARMANISM BERERRENCE 1 AITHORS BAREARYORS ATTHORS AND AND Deforce, L., Desnovers, L., Filvaroff, E., AITHORS BAREARYORS AND AND AND AND AND AND AND AND AND AND	AUTHORS BEASTIANT, DETERMINE, DESIGNATION, GROWNEL, P.J., GURNEY, A.L., Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K., Wood, W.L. and Zhang, Z.  TITLE Secreted and transmembrane polypeptides and nucleic acids encoding same JOURNAL Patent: WO 0140466-A 285 07-JUN-2001;  Genete: WO 0140466-A 285 07-JUN-2001;  Genete: WO 0140466-A 285 07-JUN-2001;  Genete: WO 0140466-A 285 07-JUN-2001;  Genete: WO 0140466-A 285 07-JUN-2001;  Genete: WO 0140466-A 285 07-JUN-2001;  Author (MS)  A	Query Match         99.8%;         Score 1532.6;         DB 6;         Length 2849;           Best Local Similarity 99.9%;         Pred. No. 0;         0;         Indels 0;         Gaps 0;           Matches 1532;         Conservative 1;         1;         Mismatches 0;         Indels 0;         Gaps 0;           Qy         4         GTAAATTCCAGTTTTCCAGCAACAAGAACAGAACAGAAC	124 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAAC	DD 607 TTGTAGAAGTTGAGGAACCCAGTGATGGAACTATATTAGGGCGCTGGTGTGGTTCTGGTA 666  304 CTGTACCAGGAAAACAGATTTCTAAAGGAAATTAGGATAAGATTGTATTGATG 363  DD 67 CTGTACCAGGAAAACAGATTTCTAAAGGAAATTAGGATAAGATTTGTATTCTGATG 726  QQ 364 AATATTTCCTTCTGAACCAGGGTTCTGCATCCACTACAACATTGTATCTGATG 726  DD 727 AATATTTCCTTCTGAACCAGGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCA 786  QQ 424 CAGAAGCTGTGAGCTACCAGGGTTCTGCATCCACTTGTCATGCCACACATTCA 786  QQ 727 AATATTTCCTTCTGAACCAGGGTTCTGCATCCACTTGTCATGCCACTGGACCTGCTTAATA 483  DD 787 CAGAAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATA 846  QQ 484 AIGCTATAACTGCCTTTGGAACCTTCAGTTTTGCCACTGGACCTGCTTAATA 846
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/mol\_type="mRNA"
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1711 ACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAAT 1770
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Materials and methods involving hybrid vascular endothelial growth factor dnas and proteins and screening methods for modulators
Patent: WO 0162942-A 148 30-AUG-2001;
LUDDWIG INSTITUTE FOR CANCER RESEARCH (US); Licentia OY (FI)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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YRCGGMCACCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEE
CDCVCRGSTGG"
2974. 2979
CCTAAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTGCTCATATTCACATATGTAA 1443
                                         2014 ACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAAT 2073
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

Toai, Y.J., Lee, R.K., Lin, S.P. and Chen, Y.H.

Identification of a novel platelet-derived growth factor-like gene, fallotein, in the human reproductive tract

Biochim. Biophys. Acta 1492 (1), 196-202 (2000)
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634 GAATTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATATTATC 693
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Stati, Y.J. Lee, R.K.K. and Lin, S.P.
Direct Submission
Submitted (14-SEP-1998) Dept. Medical Research, Mackay Memorial
Hospital, 45 Min Sheng Road, Tamshui, Taipei County 25115, Taiwan
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/note="found in female reproductive tract"
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Matches 1531; Conservative
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Db 1774 ATGTTGTATTAATAGTTCACCACTAGTTACCAGTACCACTAGC 1833  Qy 1264 TGGGTTCTGTATTCAGTTCTTCGATACGGTAATGCCAGGAAAAAA 1323  Db 1834 TGGGTTCTGTATTTCAGTTCTTTCGATACGGTAATGTCAGTACAGGAAAAAA 1893  Qy 1324 CTGTGCAAGTGACCACCTGATTCGATACGCTTAAGGTAATGTCAGTACAGGAAAAAA 1893  Qy 1324 CTGTGCAAGTGACCACCTGATTCCGTTGCTTAAGGTAATGTCAGTACAGGAAAAAA 1893  Qy 1384 CCTAAAATCGTATTACGTTTTTTTTTTTTTTTTTTCCTCATGTCCTGGG 1953  Qy 1954 CCTAAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTT	RESULT 9 AX739931 LOCUGS AX739931 LOCUGS AX739931 VERSION AX739931 VERSION AX739931 AX739931 VERSION AX739931 AX739931 AX739931 VERSION AX739931 AX739931 AX739931 AX739931 AX739931 AX739931 AX739931 AX739931 AX739931 AX739931 AX739931 AX739931 AX739931 AX739931 FIDE CORGANISM Homo sapiens Eukaryota; Marazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.  Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.  AUTHORS AUTHORS Delfani,K., Janson,A.M., Kuhn,G.H., Plate,K., Schanzer,A., Wachs,F.F. and Zhao,M. TITLE Treatment of central nervous system disorders by use of pdgf or vegf JOURNAL Neuronova AB (SE) Location/Qualifiers Location/Qualifiers Location/Qualifiers JOURNAL ADATORS Location/Qualifiers Location/Qualifiers And Lype="Genomic DDA"" Ada Arref="Laxon:9606" Ada Arref="Laxon:9606" Ada Arref="Laxon:9606" Alexandr Sila 375 c 416 g 482 t	Query Match         98.4%; Score 1511.8; DB 6; Length 1804;           Best Local Similarity         99.7%; Pred. No. 0;           Matches 1524; Conservative 1; Mismatches 3; Indels 1; Gaps 1;           Qy         4 GTAAATTCCAGTTTTCCAGCAACAAGGAACGAACGAGTACAGATCCTCAGCATGAGA 304           Db         245 GTAAATTCCAGTTTTCCAGCAACAAGGAACGAACGAAGATCCTCAGCATGAGA 304           Qy         64 GAATTATTACTGTGTCTACTAATGGAAGTTTCACAGCCCAAGGTTCCTCATACTTATC 364           Qy         124 GAAGAAATACGGTCTACTAATGGAAGTTTCACAGCCCAAGGTTCCTCATACTTATC 364           Qy         124 CAAGAAATACGGTCTTGGAAGTTTAGTAGCAGTAGAGAAATGTATGGATACAAC 424           Qy         124 TACGTTTGATGAAGAATTGGAGAATTAGTAGCAGTAAGAGAAATGTATGGATACAAC 424           Qy         184 TTACGTTTGATGAAGATTGGAGATTAGTAGCAGTAAGAGAAATGTATGGATACAAC 424           Qy         124 TACGTTTGATGAAGATTTGGAGCATTAGTAGCAGAAATGTATGGATACAAC 424           Qy         244 TTACGTTTGATGAAGAATTGGAGAACTGAAGACCCAGAAGATGAAATGTTTGGATACATTATTAGGACGAGTTTGAAGTTTTTTTT
124   CAAGAAATACGGTCTTGGTATGGAGTTAGTAGGAAAATGTATGGATACAAC		1414   CCTTCATTGATGATCCAAAGACCGGTGTCAGGGGATTGCACAAATTCACTCAC

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Homo sapiens platelet-derived growth factor C (PDGFC) mRNA, complete cds. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1804)
2 (bases 1 to 1804)
3 (bateson, D.G., Duff, M.E., West, J.W., Kelly, J.D., Sheppard, P.O., Hofstrand, P.D., Gao, Z., Sheemaker, K., Bukowski, T.R., Moore, M., Feldhaus, A.L., Humes, J.M., Palmer, T.E. and Hart, C.E. that binds to PDGF alpha and beta receptor that binds to PDGF alpha and beta receptor J. Biol. Chem. 276 (29), 27406-27414 (2001) 245 GTAAATTCCAGTTTTCCAGCAACAAGGAACAGAAACGGAGTACAAGAATCCTCAGCATGAGA 304 63 Submitted (26-APR-2000) Biomolecular Informatics, ZymoGenetics, Inc., 1201 Eastlake Avenue Bast, Seattle, WA 98102, USA GTAAATTCCAGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGA Gaps 2 (bases 1 to 1804) Gao,Z., Hatt,C., Piddington,C., Sheppard,P., Shoemaker,K., Gilbertson,D., West,J. and O'Hara,P.J. Direct Submission 1; 9; Length 1804; 3; Indels 四

1144   CTITICAGAGGAGGCCTAAAGGACAGGAAAAGGTCTTCAATCGGAAAGATTAA   144   Db   1385   CTITICAGAGGAGCCTAAAGGACAGGAAAGGTCTTCAATCGTGGAAAGTTAA   144   Cy   1204   ATGTTGTATTAAATCACTACAGTTTACAGGTTAACGCTAATCCATACCTAGC   126   Db   1445   ATGTTGTATTAAATCACTACAGTTACAGGTTAACCATACCACAGAAAAAAAA	Query Match         98.4%; Score 1511; DB 6; Length 1760;           Best Local Similarity         99.8%; Fred. No. 0;           Matches 1522; Conservative         1; Mismatches         1; Indels         1; Gaps         1;           Qy         4 GTAAATTCCAGTTTTCCAGCAACAAGAACAGAGACCAAGATCCTCAGCATGAGA         295           Db         236 GTAAATTCCAGTTTTCCAGCAACAAGAACAAGATCCTCAGCATGACAGATCCTCAGCATGAGA         295           Qy         64 GAATTATTACTGTGTCTAATGGAACTATTCACAGCCCAAGGTTTCTCTCATACTTATC         355           Qy         124 CAAGAAATACGGTCTTGGTATGGAAGTATTCACAGCCCAAGGTTTATC         355           Qy         124 CAAGAAATACGGTCTTGGTATGGAATTAGTAGCAGTAGAGGAAATGTATGGATACACA         183           Db         356 CAAGAAATACGGTCTTGGTATGGAGTTAGTAGCAGTAGAGGAAATGTATGGATACACA         183           TAACGTTTGATGAAGATTTGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACACA         183           TAACGTTTGATGAAGAATTTGGAGATTAGAGAATATGAAGAATATGAAAATGTATAGATATAGAATATAGAATATAGAAAATTAAGAATATAGAATATAAGAATATAAGAATTATAGAATATAAGAATTTAATAGAATATAAGAATTTAATAA
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PAT 10-APR-2003
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Gao, Z., Hart, C.E., Piddington, C.S., Sheppard, P.O., Shoemaker, K.E., Gilbertson, D.G. and West, J.W.
Growth factor homolog zvegf3
Growth factor homolog zvegf3
Patent: US 6528050-A 1 04-MAR-2003;
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KEYMORDS KEYMORDS KEYMORDS Homo sapiens (human) ORGANISM Homo sapiens Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  AUTHORS AUTHORS Gilbertson, D.G. AUTHOR Authors I. 1760 AUTHOR COS TITLE Method of treating fibrosis Location/Qualifiers I. 1760 Lype="genomic DNA" AD_Xref="taxon:9606" AD_Lype="genomic DNA" AD_Lype="genomi	Query Match 98.4%; Score 1511; DB 6; Length 1760; Best Local Similarity 99.8%; Pred. No. 0; Matches 1522; Conservative 1; Mismatches 1; Indels 1; Gaps 1;	Qy 4 GTAAATTCCAGTTTTCCAGCAACAGAACAGAACAGAGTACAAGATCCTCAGCATGAGA 63	Qy 64 GAATTATACTGTGTCTACTBATGGAAGTATTCACAGGCCCAAGGTTTCCTCATACTTATC 123  Db 296 GAATTATTACTGTGTCTACTAATGGAAGTATTCACAGGCCCAAGGTTTCCTCATACTTATC 355	QY         124 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAAC 183           DD         356 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGGAAAATGTATGGATACAGTAGAAAATGTATGGATACAGTAGAAAATGTATGGATACAGTAGAAAATGTATGAAC 415	Qy 184 TTACGTTTGAAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATT 243	Qy 244 TIGIAGAAGTIGAGGAACCCAGTGATGGAACTATATAGGGGGGTGGTGTGGTTCTGGTA 303	QY 304 CIGIACCAGGAAAACAGATITCIAAAGGAAATCAAATIAGGATAAGATTTGTATCTGATG 363  Db 536 CIGIACCAGGAAAACAGATTTCTAAAGGAAAICAAAITAGGATAAGATTTGTATCTGATG 595	QY         364 AAIAITTTCCTTCTGAACCAGGGTTCTGCATCCACTACAACATTGTCATGTCAACAATTCA 423           DD         596 AAIATTTCCTTCTGAACCAGGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCA 655	Qy         424 CAGAAGCTGTGAGTCCTTCAGTGCTACCCCTTCAGCTTTGCCACTGGACCTGCTTTAATA 483           Db         656 CAGAAGCTGTGAGTCCTTCAGTGCTACCCCTTCAGCTTTGCCACTGGACCTTCATAATA 715	QY         484 AIGCIAIAACIGCCTITAGIACCTIGAAGACCTIAITCGAIAICTIGAACCAGAGAGI 543           DD         716 AIGCIAIAACIGCCTITAGIACCTIGGAAGACCTIAITCGAIAICTIGAACCAGAGAGI 775           QY         544 GGCAGITGGACTIAGAAGATCTAIAIAGGCCAACTICTIGGCAAGGCTITIG 603
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AB033831 1817 bp mRNA linear PRI 26-JUL-2000 Homo sapiens hSCDGF mRNA for spinal cord-derived growth factor, complete cds.
AB033881

DEFINITION

ACCESSION

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                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 1817)
Hamada, T., Ui-Tei,K. and Miyata,Y.

Birect Submission
Submitted (25-OCT-1999) Tsuyoshi Hamada, Nippon Medical School,
Department of Pharmacology; 1-1-5, Sendagi, Bunkyo-ku, Tokyo
113-8602, Japan (E-mail:t-hamada@nms.ac.jp,
Tel:81-3-3822-2131(ex.5277), Fax:81-3-5814-1684)

Location/Qualifiers

1 1.187
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   spinal cord-derived growth factor; scdgf gene
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                                                                                                                                                                               Hamada,T., Ui-Tei,K. and Miyata,Y.
A novel gene derived from developing a
unique member of the PDGF/VEGF family
20317014
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1. 1817
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/gene="hSCDGF"
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Homo sapiens
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364 AATATTTCCTTC'           769 AATATTTTCCTTC'	AATATTTTCCTTCTGAACCAGGGTTCTGCATCACACAATGTCATGCCACAATTCA 423 	
424 CAGAAGCTGTGAGTC	GTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATA 483	
484 ATGCTATAACTGC 	AACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGAT 543	
544 GGCAGTTGGACTT 	GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG 603 	m
604 TTTTTGGAAGAAA 1009 TTTTTGGAAGAAA	TITITIGGAAGAAAICCAGAGIGGIGGAICIGAACCTICIAACAGAGGAGGAGGIAAGAITAI 663 	m
664 ACAGCTGCACACC	CTGTAACTTCTCAGTGTCCATAAGGAAGAACTAAAGAGAACGATA 723 	m
724 CCATTTTCTGGCC 	SCCAGGTTGTCTCCTGGTTAAACGCTGTGGGAACTGTGCCTGTTGTC 783	m
784 TCCACAATTGCAA                1189 TCCACAATTGCAA	CAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACCACGAGG 843 	m
844 TCCTTCAGTTGAGAG 	GACCAAASACCGGTGTCAGGGGATTGCACAAATCACTGACCGACGTGG 903 	<b>m</b>
904 CCCTGGAGCACCA              1309 CCCTGGAGCACCA	CATGAGGAGTGTGACTGTGTGCAGAGGAGCACAGGAGGATAGCCGC 963	m
964 ATCACCACCAGCA()	CAGCAGCTCTTGCCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAA 1023	m m
1024 CGTATGCGTTATC             1429 CGTATGCGTTATC	ATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAG 1083	
1084 GATTTACAGTGCA              1489 GATTTACAGTGCA	114	m m
1144 CTTTTGAGAGGACC 	GGCCTAAAGGACAGGAGAAAGGTCTTCAATCGTGGAAAGAAA	m m
1204 ATGTTGTATTAAA'                1609 ATGTTGTATTAAA	atgitgibitabapiagatcaccagcibafiticagagitaccaig-tacgtaticcactag 1262 	N
1263 CTGGGTTCTGTAT 	GTATTTCAGTTCTTTCGATACGGCTTAGGGTAAT-GTCAGTACAGGAAAA 1321 	-1 M
1322 AACTGTGCAA 	CTGTGCAAGTGAGCACCTGATTCCGTTGCTTAACTCTAAAGCTCCATGTC 1378	m m
1379 CTGGGCCTAAAAT                1789 CTGGGCCTAAAAT	CCTAAAATCGTATAAATCTGGAT 1407 	

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Search completed: November 26, 2003, 03:42:37 Job time: 3799.28 secs

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Copyright (c) 1993 - 2003 Compugen Ltd.
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#### ALIGNMENTS

BP

AAA12524 standard; cDNA; 1536

RESULT 1

AAA12524

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The present sequence encodes a human platelet-derived growth factor C (PDGP-C) (formally designated VBGP-F) fragment. PDGP-C polypeptides have the ability to stimulate and enhance proliferation or differentiation, and/or growth or motility of cells expressing a PDGP-C receptor.

CC PDGP-C polypeptides can be used in pharmaceuticals for promoting cell proliferation, preferably in combination with one other growth factor and heparin. Pharmaceuticals comprising PDGP-C polypeptides can also be used for stimulating connective tissue or wound healing. The PDGP-C polypeptide can be enzymatically processed to generate the active truncated form of PDGP-C and used to regulate the receptor-binding specificity of PDGP-C. PDGF-C can also be used to promote fibroblast mitogenesis in a mammal and to induce PDGF alpha receptor activation.

CC pDGP-C antagonists can be used to inhibit tumour growth of a tumour expressing PDGF-C in amammal. Specific types of human tumours, e.g. choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma and erythroleukemia, can be identified by testing for expression of PDGF-C antagonists can also be used to inhibit tissue cremodalling during invasion of tumour cells into a normal population of especially found in the lung, kidney or liver.
                                                                                                                                                                                                                                                                                               Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation, differentiation, growth and motility of cells expressing the PDGF-C
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Betsholz C;
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UNIV HELSINKI LICENSING LTD
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98US-0113002.
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Heldin C,
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P-PSDB; AAY84558.
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03-DEC-1998;
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15-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes the isolation of a novel human vascular endothelial cell growth factor-E (VEGF-E) polypeptide which has crandothelial cell growth factor-E (VEGF-E) polypeptide which has crandothelial cell growth factor-E (VEGF-E) can be administered therapeutically, especially by expressing encoding polynucleotides, to treat cardiovascular or endothelial disorders in mammals, especially commanders in wammals, especially commanders in mammals, especially commanders in wammals, especially commanders in mammals, especially can be combined with a carrier in pharmaceutical compositions, which can be administered to treat disorders as above. VEGF-E can be used to creat angiogenic disorders in mammals (especially humans) e.g. cancer or age-related macular degeneration. It can be used to generate antibodies, useful therapeutically as antagonists, as above. The antibodies are also useful to detect VEGF-E polypeptide, especially to diagnose cardiovascular, endothelial or angiogenic disorders in mammals (e.g. vascular disease, or neovascularization associated with tumor formation, by contacting the antibody with a tissue sample and detecting formation of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding VEGF-E can be used to diagnose cardiovascular and endothelial disorders in mammals, by detecting abnormally high or low VEGF-E gene expression in the mammals, by detecting abnormally high or low VEGF-E gene expression in the susceptibility to a disease related to a mutated form of VEGF-E or
  1441 TAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATG 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                              VEGF-E; human, vascular endothelial cell growth factor; wound repair;
treatment; cardiovascular disorder; endothelial disorder; therapy;
tissue generation; regeneration; cardiac hypertrophy; cancer; detection;
angiogenic disorder; age-related macular degeneration; vascular disease;
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                                                                            AATTAAACTTGTGTCATGCTGATAGGACAGACTGGA 1536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neovascularization; tumor; gene mapping; ss
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259..1296
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/product= "VEGF-E"
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cardiovascular, endothelial or angiogenic disorder such as a tumor), by detecting a mutation in the VEGF-E-encoding sequence isolated from a sample. They may also be used to produce probes useful to detect related sequences or for gene mapping. This sequence encodes the human VEGF-E
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                                                                                                                                                 protein described in the method of the invention.
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Pred. No. 0;
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243 580 303 640 363 423 760 483 820 543 880

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Human, PRO; EST; expressed sequence tag; PCR primer; hybridisation; probe; blood coagulation disorder; cancer; cellular adhesion disorder; secreted protein; transmembrane protein; ss.
                           Human PRO200 nucleotide sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulartion disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AAZ33391 to AAZ34338, and AAY41685 to AAY41774 represent polymucleotide and polypeptide sequence given in the exemplification of the present
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                                                                                      AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polynechides and polypeptides have cytostatic activity. The PRO polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bioactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bioactive molecules to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
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Novel PRO polypeptides and polynucleotides used in detection methods, to target bioactive molecules to specific cells, and to modulate cellular activities -
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                                                                                                                                                                                                                                                                                                      Score 1532.6;
Pred. No. 0;
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E, Fong S, Gao W, Gerber H, Gerritsen ME;
PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
Napier MA, Pan J, Paoni NF, Roy MA;
TA, Tumas D, Williams PM, Wood WI;
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Godowski PJ,
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Goddard A, G
Kljavin IJ,
Shelton DL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kabakoff RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel PRO polypeptides useful for preventing or rescuing retinal cells from injury caused by ocular diseases such as retinitis pigmentosa, retinopathy, retinal degenerative diseases, degenerative myopia, uveltis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTAAATTCCAGTTTTCCAGCAACAAGAACAGAACGGAGTACAAGATCCTCAGCATGAGA
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Kuo SS, La Fleur M,
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Matches 1532; Conservative
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Klein RD, Kljavin IJ,
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                    <u>CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGGAAAAATGTATGGATACAAC</u>
                                                        CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KP, Goddard A, Gurney AL, Hebert C, Henzel W;
Pan J, Pennica D, Shelton DL, Smith V;
, Watanabe CK, Wood WI, Yan M;
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20-DEC-1999; 99WO-US30999.
30-DEC-1999; 99WO-US31274.
05-JAN-2000; 2000WO-US00219.
06-JAN-2000; 2000WO-US00277.
06-JAN-2000; 2000WO-US00376.
11-FEB-2000; 2000WO-US03565.
18-FEB-2000; 2000WO-US03341.
                  99WO-US21090.
99WO-US21090.
99WO-US21547.
99WO-US23089.
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RC, Lu Y, Pan
TA, Tumas D, Wa
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P-PSDB; AAB33414.
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01-DEC-1999;
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02-DEC-1999;
                  13-SEP-1999;
15-SEP-1999;
15-SEP-1999;
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Stewart TA,
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TTTTTGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTAT 1026
                                                                                                                          The present invention describes nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or anglogenic disorder in mammals by modulating cell proliferation, anglogenic disorder in mammals by and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or anglogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCS) and vectors associated with decreased PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB2438 to AAB4438 to AAB4435 represent nucleotide and protein sequences used in
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                                                                                                                                                                                                                                                                                                                                                                                Score 1532.6;
Pred. No. 0;
1; Mismatches
                                                                                                    Claim 61; Fig 49; 315pp; English
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Matches 1532; Conservative
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 ATGTTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGC 1263
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Kuo SS, Paoni NF, Smith V;
                   ATGTTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGC
                                                                                                                                                                                         TGGGTTCTGTATTTCAGTTCTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAA
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Klein RD, F
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99US-011554.
99US-0123957.
99US-0134445.
99US-0134287.
99US-0131252.
99US-0144758.
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Gurney AL, Kl
Williams PM, 1
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99WO-US21547
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Watanabe CK, V
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08 MAR 1999

12 - MAR 1999

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breast; prostate; cervical; tumour necrosis factor-alpha; INF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy; ss.

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Human secretory and transmembrane; PRO; mammalian; cancer; lung;

encoding for PRO200 polypeptide.

Human cDNA sequence

(first entry)

24-OCT-2001

AXAXAXAX XXXXXX

AAS21386;

BP

AAS21386 standard; cDNA; 2849

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AAS1244-AAS21518 encode for novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bloactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TMF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cartilage, the proliferation of inner ear utricular supporting cells or
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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2000WO-US03565.
2000WO-US04341.
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molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
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                                                   Score 1532.6; Pred. No. 0; 1; Mismatches
                                    Sequence 2849 BP; 851 A; 528 C;
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Best Local Similarity 99.9%;
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1143 1203 1626 1746 1443 Human; PRO; cardiant; antiangiogenic; antiarteriosclerotic; hypotensive; vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic; vulnerary; antianginal; gene therapy; cardiovascular disease; endochelial disorder; angiogenic disorder; cancer; periodontal disease; GATTTACAGTGCATTCTGAAAGAGGAGACATCAAAACAGAATTAGGGGTTGTGCAACAGCT CGTATGCGTTATCTCCATCTTAATCTTAGTTTTCAAGGACCTTTCATCTTCAG ATGITGIATIAAATAGATCACCAGCIAGTITCAGAGTTACCATGTACGTATCGATTCACTAGC 1264 TGGGTTCTGTATTTCAGTTCTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAA TGGGTTCTGTATTTCAGTTCTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAA CTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACTCTAAAGCTCCATGTCCTGGG crerecaadreaccaccrearrecerrecerrectraacreraagcrecarerecege CGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAG GATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCT ATGITGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGC ACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAAT TAPACTIGICALGATAGGACAGACTGGA 1899 TAAACTTGTGTCATGCTGATAGGACAGACTGGA 1536 99WO-US12252. 99US-0144758. 99US-0145698. 99US-0145622. 99WO-US20111. 2000WO-US13705 entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is one of seventeen nucleic acids encoding PRO polypeptides. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating cardiovascular, endothelial or antigonic disorders in a mammal. Examples of these disorders include cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and antagonists are also used to prevent tumour angiogenesis and for treating periodontal diseases. They are also used to stimulate wound healing and tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO antibodies are useful for diagnosing a cardiovascular, endothelial or angiogenic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGGAGAAAATGTATGGATACAAC
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                                                                                                                                                                                                                                                                                                                                                                         Seventeen nucleic acids encoding PRO polypeptides which are useful in diagnosis and treatment of cardiovascular, endothelial or angiogenic disorders in a mammal -
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Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters
Pitti RM, Watanabe CK, Williams PM, Wood WI;
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Pred. No. 0;
1; Mismatches
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 30-NOV-1999; 99WO-US28409.
02-DEC-1999; 99WO-US28565.
16-DEC-1999; 99WO-US33565.
11-FEB-2000; 2000WO-US03565.
18-FEB-2000; 2000WO-US04341.
24-FEB-2000; 2000WO-US04342.
24-FEB-2000; 2000WO-US05044.
02-MAR-2000; 2000WO-US05841.
10-MAR-2000; 2000WO-US05841.
15-MAR-2000; 2000WO-US05834.
21-MAR-2000; 2000WO-US05834.
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Matches 1532; Conservative
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Paoni NF, Pitti RM,
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P-PSDB; AAB50952.
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1147 TCCACAATTGCAATGAATGTCAATGTGTCCCCAAGCAAAGTTACTAAAAAAATACCACGAGG 1206
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                 TTACGTTTGATGAAAGATTTGGCCTTGAAGACCCAGAAGATGACATATGCAAGTATGATT
                                                                              TIGITAGAAGTIGAGGAACCCAGTGAAGGAACTATATTAGGGCGCTGGTGTGTCTGGTA
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                                                                                                                      CTGTACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                          Human, PRO526, PRO719, PRO200, PRO725, PRO1031, immune related disease, inflammation, thyroiditis, demyelinating disease, skin disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PR0200
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              TAAACTTGTGTCATGCTGATAGGACAGACTGGA 1899
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99.8%; Score 1532.6;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1532; Conservative 1; Mismatches
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Wood WI;
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                                                                                                       AAC88962 standard; cDNA; 2849
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Kuo SS,
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                                                                                                                ACCAGAACATICTATGTACTACAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAAT 1866
                                                                                                                                                                                                                                                             Human; angiogenesis-associated protein; PRO; endothelial cell growth; cardiac hypertrophy; cardiovascular disorder; endothelial disorder; angiogenic disorder; atherosclerosis; osteoporosis; hypertension; myocardial infarction; diabetic retinopathy; rheumatoid arthritis; Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer; Alzheimer's disease; Huntington's disease; stroke; drug screening; gene therapy; transgenic animal; ss.
                                CTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACTCTAAAGCTCCATGTCCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P. Ferrara N, Gerber H, Goddard A;
L, Hillan KJ, Kuo SS, Mark MR, Marsters SA;
Watanabe CK, Williams PM, Wood WI;
                                                                                                                                                                                                                                               Human angiogenesis-associated protein PRO200 cDNA, SEQ ID NO:50.
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Pitti RM,
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P-PSDB; AAB53074.
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14-MAY-1999;
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23-JUN-1999;
20-JUL-1999;
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15-SEP-1999;
15-SEP-1999;
05-OCT-1999;
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Paoni NF, P
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PT New isolated nucleic acid for producing a PRO polypeptide, analyzing genetic disorders and treating cardiovascular, endothelial or angiogenic disorders unch as atherosclerosis, wounds or cancer.

XX Claim S8; Fig 21A-B; 293pp; English.

XX Claim S8, Fig 21A-B; 293pp; English.

XX Claim S8, Fig 21A-B; 293pp; English.

XX Crhe invention relates to novel human angiogenesis-associated proteins designated PRO proteins (AAB3104-B53097), and to nucleic acids encoding PRO proteins (AAB3104-B53097), and to nucleic acids encoding PRO protein, against a proportion of a PRO protein, against a protein, fusion protein, and compounds which inhibit the expression of a PRO protein, additionally encompasses methods of identifying modulators of PRO protein, additionally encompasses methods of identifying modulators of PRO additionally encompasses methods of identifying modulators of PRO additionally encompasses methods of identifying modulators of PRO additionally encompasses methods of identifying modulators of PRO additionally encompasses methods of identifying modulators of PRO additionally encompasses methods of identifying modulators of PRO additional triasue; treating a cardiovascular, endothelial or angiogenic disorder via the administration of a PRO protein, PRO protein, PRO administration of a PRO protein, an entagonist procession of an entagonist procession of an entagonist procession of an entagonist procession of an entagonist procession of an entagonist procession of an entagonist procession of an entagonist procession of an entagonist procession of an entagonist procession of an entagonist procession of an entagonist procession of an entagonist procession of an entagonist procession of an entagonist procession of an entagonist procession of an entagonist production of PRO proteins, and an entagonist production of PRO proteins, and pure and an entagonist production of PRO proteins, and pure and penses encoding PRO proteins, to analyse genes encoding PRO proteins, to analyse genes encoding PRO proteins, to analyse
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Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;

Query Match
Best Local Similarity 99.9%; Pred. No. 0;

Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps

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CAGAAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATA 483

AATATTTTCCTTCTGAACCAGGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCA

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Human; PRO polypeptide; secreted and transmembrane protein; tumour necrosis factor-alpha; TNF-alpha; blood; proliferation; differentiation; chondrocyte; tumour; genetic disorder;
 1867 TAAACTTGTGTCATGCTGATAGGACAGACTGGA 1899
                                                                                                                         cDNA encoding human PRO polypeptide #143
                                                       BP.
                                                      ACA03745 standard; cDNA; 2849
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2000WO-US04341.
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99WO-US30095.
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12-UN-1998;
14-UN-1998;
10-SEP-1998;
14-SEP-1998;
14-SEP-1998;
14-SEP-1998;
16-SEP-1998;
07-OCT-1998;
29-OCT-1998;
29-OCT-1998;
05-UMOV-1999;
06-UMAR-1999;
10-MAR-1999;
10-MAR-1999;
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20-APR-1999;
05-APR-1999;
20-APR-1999;
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15.SEP-1999;
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05.OCT-1999;
29.NOV-1999;
30.NOV-1999;
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22-DEC-1999;
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                                  ATGCTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAAT
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for modulating biological activities of cells expressing PRO polypeptides, and for identifying agonists or antagonists.

The PRO polypeptides are useful for for stimulating the release of tumour necrosis factor (TMF)-lapha from human blood, for stimulating the proliferation or differentiation of chondrocytes, and detecting the presence of tumours. The polymucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, for the genetic analysis of individuals with genetic disorders, and in gene therapy. ACA03803-ACA03877 represent cDNAs encoding the human PRO polypeptides of the invention.

Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at
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99.8*; Score 1552.0,
Best Local Similarity 99.9*; Pred. No. 0;
Matches 1532; Conservative 1; Mismatches
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# (GETH ) GENENTECH INC.

Gao W; Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, G: Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

### WPI; 2003-331925/31. P-PSDB; ABU66988.

New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or cancer

# Claim 2; Fig 285; 659pp; English.

The invention relates to an isolated nucleic acid comprising, or which is at least 80% identical to, or the full-length coding sequence of, any of the 275 nucleotide sequences, encoding the corresponding PRO polypeptide (one of 275 secreted or transmembrane proteins). The nucleic acid further comprises the full-length coding sequence of the DNA deposited cunder American Type Culture Collection (ATC) accession number in a list given in the specification. Also included are vectors and host calls for producing PRO proteins, PRO fusion proteins, anti-PRO attibodies, PRO extracellular domains and mature sequences, methods of detecting PRO proteins, methods for stimulating the release of TNF-alpha (tumour necrosis factor alpha) from human blood, and the proliferation of differentiation of fondrocyte cells, the comparation of, or gene expression in pericyte cells, the release or proteoglycans from cartilage, proliferation of finer ear urticular cultor proliferation of mononuclear cells, the release of proliferation of endothelial cells, a method for modulating the uptake of glucose or free fatty acid (FFA) by skeletal muscle cells, cor the differentiation of adipocyte cells, a method for modulating the proliferation of adipocyte cells, a method for inhibiting the bluding of A-pepting to factor VIIA, or the differentiation of adipocyte cells, a method for detecting the proliferation of adipocyte cells, a method for detecting the proliferation of adipocyte cells, a method for detecting cor the differentiation of adipocyte cells, a method for detecting cor presence of a tumour in a mammal and an oligonucleotide probe derived for multiples are useful for treating inflammatory diseases, organ collypeptides are useful for treating inflammatory diseases, organ promature aging, AIDS (acquired inpury, infertility, birth defects, or premature aging, AIDS (acquired inpury, infertility, birth defects) or premature aging, AIDS (acquired inpurs).

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                                                                    CGTATGCGTTATCTCCATCCTTAATCTCAGTTGCTTCAAGGACCTTTCATCTTCAG 1083
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                                                                                                         GATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCT
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## (GETH ) GENENTECH INC.

Gao W; Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gr Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-148238/14. P-PSDB; ABU59793.

Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer treatments

Claim 2; Fig 285; 659pp; English

The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in collypeptides are useful in detecting PRO polypeptides in a sample, in collypeptide abloactive molecule to a cell expressing a PRO polypeptide. PRO polypeptide and propertion in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus conseful for treating cardiac insufficiency disorders. PRO156, and PRO136, PRO943, PRO928, PRO926, PRO1366 and PRO1387 induce c-fos in endothelial growth, and PRO536, PRO943, PRO928, PRO926, PRO943, PRO926, PRO1386 or PRO536, and artagonist of this polypeptide are useful for treating conditions or disorders where angiogenesis would be charting cancerous tumours. PRO821 inhibits vascular candothelial growth factor (VEGF) stimulated proliferation of endothelial colls and is thus useful for inhibiting andothelial cell growth. PRO926, PRO1168, PRO1184 and PRO1375 stimulated proliferation of calls which would be beneficial in inhibiting tumour growth. PRO826, PRO1168, PRO1184, PRO91346 and PRO1375 stimulated proliferation of catinal neurons cells (PRO9132) is also enhances survival (por infared proliferation of descreased mesangial cells) and therefore are useful for treating kidney disorders associated with dermatitis, herpetiformis or crohn's disease. PRO9110, PRO944, PRO91312, PRO9193 and proliferation and/or redifferentiation of chondrocytes in culture and enterpress and are thus useful for treating sports inhighties, and are thuse associated with dermatitis, herpetelformis or crohn's disease. PRO9110, proved and profile and profil sequence encodes a novel human PRO protein.

GACCTTTCATCTTCAG 1083  GACCTTTCATCTTCAG 1446  GAGTTGTGCAACAGCT 1143  GGTGGAAAGAAATTAA 1203  CGTGGAAAGAAATTAA 1203	CCATGTACGTATTCCACTAGC 1263	AAGCHCCATCTCTGGG 1746 CATATTCACATATGTAA 1443 CATATTCACATATGTAA 1806 ACTATGTTGCTATGAAT 1503 ACTATGTTGCTATGAAT 1866 ACTATGTTGCTATGAAT 1866
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 ORGANISM: Human
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US-09-457-06-36

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Maximum Match 100%
Listing first 45 summaries
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             GenCore (c) 1993
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APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
APPLICANT: Kuo, Sophia S.
TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR
TITLE OF INVENTION: ENDOTHELIAL CELL GROWTH FACTOR AND BONE MCREHOGENETIC
TITLE OF INVENTION: PROTEIN 1 AND NUCLEIC ACIDS ENCODING SAME, THEIR USES,
TITLE OF INVENTION: AND PROCESSES FOR THEIR PRODUCTION
FILE REPERENCE: PL122
CURRENT APPLICATION NUMBER: US/09/040,220D
CURRENT FILING DATE: 1998-03-17
NUMBER OF SEQ ID NOS: 8
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US-09-099-041A-1
US-09-209-041A-1
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; Patent No. 6391311
; GENERAL INFORMATION:
LOCATION: 2689
OTHER INFORMATION: N is A,
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Db 1721 CCTAAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTT		TITLE REFERENCE: P1122P2 ; FILE REFERENCE: P1122P2 ; CURRENT APPLICATION NUMBER: US/09/265,686 ; CURRENT FILING DATE: 1999-03-10 ; PRIOR APPLICATION NUMBER: US 09/040,220 ; PRIOR FILING DATE: 1998-03-17 ; PRIOR FILING DATE: 1998-03-17 ; PRIOR APPLICATION NUMBER: US 09/184,216	01	ORGANISM: Human FEATURE: NAME/KEY: Unknown LOCATION: 2689	Any nucleo	Best Local Similarity 99.9*; Pred. No. 0; Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Qy 4 GTAAATTCCAGTTTTCCAGCAACAAGGAACAGAACAGAA	Db 341 GTAAATTCCAGTATTTCCAGCAACGAACGAACGAACGAGTACAAGATCCTCAGCATGAGA 400 OV 64 GAATTATTATTACTAGTAATGAAAGTATTCACAGCACCAAGGTTTCCTCATAATTATATTATTATATATA	401 GAATTAITTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATC 124 CAAGAAATAGGTCTTGGTATGGAGATTAGTAGGAGAAGAAGAAAATGTATGGATACAAC	Db 461 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGT	Db 521 TTACGTTTGARGAAGTTTGGAGCTTGAAGACCCAGAAGATGACATATGCAAGTATGCAAGTATGATT 580 Qy 244 TTGTAGAAGTTGAGGAACCCAGTGATGGAACTATATTAGGGGCGCTGGTGGTGTTCTGGTA 303	581 TTGTAGAAGTTGAGGAACCCAGTGATGGAACTATATAGAGGGGGTGGTGGTGGTTCTGGTA 304 CTGTACCAGGAAAACAGATTTCTAAAGGAATTAGGAATATGGATAGATA	641 CTGTACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATG 364 AATATTTTCCTTCTGAACCAGGGTTCTGCATCCACTACAACATGTGATGCAAATTCCACAATTCA		761 CAGAAGCTGTGAGTCCTTCAGTGCTACCCCTTCAGCTTTGCCACTGGACCTGCTTAATA 82
	Qy         484 ATGCTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGT 543           Db         821 ATGCTATAACTGCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACAGAGAT 880           Qy         544 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTCTTGGCAAGGCTTTG         603           Db         881 GGCAGTTGGAACATTTAGAAGATCTATATAGGCCAACTTCTTGGCAAGGCTTTTG         603           Db         881 GGCAGTTGGAACATTTAGAAGATCTATATAGGCCAACTTTGGCAACTTCTTGGCAAGGCTTTTG         940	604 TTTTGGAAGAAATCCAGAGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTAT	Oy 724 COATTTCTGGCCAGGTTGTCTCTGGTTAAACGCTGTGGGGAACTGTGCTGTGTCTGTTGTC 783  Db 1061 CCATTTCTGGCCAGGTTGTCTCTGGTTAAACGCTGTGGGGAACTGTGCTTGTC 7120	OY 784 TCCACAATTGCAATGTCAATGTCTCCCAAGCAAAGTTACTAAAAATACCACGAGG 843	OY 844 TCCTTCAGTTGAGACCAAASACCGGTGTCAGGGGATTGCACAAATCACCCGACGTGG 903	QY         904         CCCTGGAGCACCATGAGGAGTGTGACAGTGTGCAGAGGAGCACAGGAGGATAGCCGC         963           DD         1241         CCCTGGAGCACCATGAGAGTGTGACTGTGTGTGCAGAGGAGCACAGGAGGATAGCCGC         1300	Qy         964         ATCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCAGTG	1024	OY 1084 GATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCT 1143	Qy 1144 CTTTTGAGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAA	Qy 1204 AIGTIGTAITAAATAGAICACCAGCTAGTITCAGAGTTACCATGTACGTAITCCACTAGC 1263	Qy 1264 TGGGTTCTGTATTTCAGTTCTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAA 1323 	Qy         1324         CTGTGCAAGTGAGCACCTGATTCCGTTGCTTTAACTCTAAAGCTCCATGTCCTGGG         1383           Db         1661         CTGTGCAAGTGAGCACTGATTCCGTTGCCTTAACTCTAAAGCTCCATGTCCTTGG         1720	CCTAAAATCGTATAAAATCTGGATTTTTTTTTTTTTTGCTCATATTCACATATGTAA

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                           | Sequence 32, Application US/09564595D |
| Sequence 32, Application US/09564595D |
| Patent No. 6495668 |
| GENERAL INFORMATION: |
| APPLICANT: Gilbert, Teresa |
| APPLICANT: Hart, Charles E. |
| APPLICANT: Hart, Charles E. |
| APPLICANT: Hart, Charles E. |
| APPLICANT: Hart, Charles E. |
| APPLICANT: Hart, Charles E. |
| TILE REFERENCE: 99-19 |
| CURRENT APPLICATION UNMBER: US/09/564,595D |
| CURRENT FILING DATE: 1999-06-03 |
| PRIOR APPLICATION NUMBER: US 60/180,169 |
| PRIOR APPLICATION NUMBER: US 60/180,169 |
| PRIOR PILING DATE: 1999-11-10 |
| PRIOR PRILING DATE: 2000-02-04 |
| NUMBER OF SEQ ID NOS: 57 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SENGIN 1760 |
| LENGTH: 1760 |
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Best Local Similarity 99.8
Matches 1522; Conservative
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; LOCATION: (154)...(1191)
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ORGANISM: Homo sapiens
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                         ATGCTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGAT
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APPLICANT: Sheppard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Glibertagon, Debra G.
APPLICANT: Glibertagon, Debra G.
TITLE OF INVENTION: GROWTH PACTOR HOMOLOG ZVEGF3
FILE REFERENCE: 98-60C1
CURRENT APPLICATION NUMBER: US/09/706,968
CURRENT FILING DATE: 2000-11-06
PRIOR APPLICATION NUMBER: US/09/541,752
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PRIOR SPLICATION NUMBER: US/09/541,752
PRIOR SEQ ID NOS: 50
SOFTWARE: FRESEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1760
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98.4%; Score 1511; D
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1522; Conservative 1; Mismatches
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APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher
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                   CGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAG 1083
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    CCATTITCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGGGAACTGTGCCTGTTGTC
                                                                                                               TCCTTCAGTTGAGACCAAASACCGGTGTCAGGGGATTGCACAAATCACTCACCGACGTGG
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Patent No. 6432673

GENERAL INFORMATION:
APPLICANT: Baco, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
TITLE DO INVANTION: GROWTH FACTOR HOMOLOG ZVE)
TITLE REFERENCE: 98-60
CURRENT APPLICATION NUMBER: US/09/457,066

CURRENT FILING DATE: 1999-12-07
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us-09-852-209a-4.rni

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CCCTGGAGCACCATGAGGAGTGTGACTGTGTGCAGAGGAGGAGCACAGGAGGATAG 1077
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                                                                                                                    GAATTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATC
                                                                                                                                   GAATTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATC
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                                                           GTAAATTCCAGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGA
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                              Gaps
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 Length 1095;
                             Indels
Score 955.6; DB 4;
Pred. No. 9.8e-259;
1; Migmatches 0;
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; Patent No. 6528050
 Query Match
Best Local Similarity 99.9%;
Matches 955; Conservative
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                                                                                    ATCACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGT----GCAGTGGCTGATTCTATTAG
    ZVEGF3
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Patent No. 6422673

GENERAL INFORMATION:

APPLICANT: Hart, Charles E.

APPLICANT: Bladington, Christopher S.

APPLICANT: Shepmard, Paul O.

APPLICANT: Shepmard, Paul O.

APPLICANT: Glabertson, Debra G.

APPLICANT: Glabertson, Debra G.

APPLICANT: Glabertson, Debra G.

APPLICANT: Glabertson, Debra G.

APPLICANT: Glabertson, Debra G.

APPLICANT: West, James W.

TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVB.

CURRENT APPLICATION NUMBER: US/09/457,066

CURRENT FILIAGO DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 50

SOFTWARE: FASESQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
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LENGTH: 1095
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US-09-457-066-50
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GAATTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATC 123
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46.9%; Score 721; DB 4; Length 35
Best Local Similarity 83.6%; Pred. No. 1.4e-192;
Matches 817; Conservative 0; Mismatches 160; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 34, Application US/09564595D
Patent No. 649568
GENERAL INPORMATION:
APPLICANT: Gilbert, Teresa
APPLICANT: Gilbert, Teresa
APPLICANT: Gilbert, Teresa
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564.595D
CURRENT APPLICATION NUMBER: US/09/564.595D
CURRENT APPLICATION NUMBER: US 09/304,216
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
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SPRIOR FILING DATE: 1999-11-10
SPRIOR FILING DATE: 1999-11-10
SPRIOR PAPLICATION NUMBER: US 60/180,169
SPRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTHARE: FASTSEQ FOR WINGOWS VEFSION 4.0
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; LOCATION: (1049)...(2086)
US-09-564-595D-34
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                              APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
TILLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILLE REFERENCE: 98-601
CURRENT FILING DATE: 2000-11-06
PRIOR FILING DATE: 2000-33-31
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PastsEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGGGAACTGTGCCTGTTGTC
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                                                                                                                                                              Gaps
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0
                                                                                                                Length 3571;
                                                                                                                                                              Indels
                                                                                                                Score 721; DB 4; I
Pred. No. 1.4e-192;
0; Mismatches 160;
                                                                                                             Query Match

Best Local Similarity 83.6%;
Matches 817; Conservative
; FEATURE:
; NAMBKEX: CDS
; LOCATION: (1049)...(2086)
US-09-706-968-42
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                                                                                                                                                                        TITITIGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTAT
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patent No. 6432673

general INPORMATION:
APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Hart, Charles E.
APPLICANT: Sheepard, Paul O.
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i_LCCATION: (1)...(1035)
COTHER INFORMATION: n = A,T,C or G
US-09-457-066-6
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US-09-457-066-6
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Pred. No. 1.4e-192;
0; Mismatches 160; Indels
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APPLICANT: Gao, Zeren
APPLICANT: Piddington, Christopher S.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Games W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REFERENCE: 98-60
CURRENT APPLICATION NUMBER: US/09/457,066
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 42, Application US/09457066
Patent No. 6432673
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                            964 ATCACCACCAGCAGCTC 980
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Best Local Similarity 83.6%;
Matches 817; Conservative
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; LOCATION: (1049)...(2086)
US-09-457-066-42
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44.6%; Score 684.4; DB 4;
Best Local Similarity 57.5%; Pred. No. 1.5e-182;
Matches 547; Conservative 239; Mismatches 166;
CURRENT APPLICATION NUMBER: US/09/706,968
CURRENT FILING DATE: 2000-11-06
PRIOR APPLICATION NUMBER: US/09/541,752
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO
                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                 LENGTH: 1035
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                                                                                                                   CAGAAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATA 483
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 GNATHATHACNGTNWSNACNAAYGGNWSNATHCAYWSNCCNMGNTTYCCNCAYACNTAYC 202
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                                    CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAAC
                                                          CMGNAAYACNGTNYTNGTNTGGMGNYTNGTNGGCNGTNGARGARAAYGTNTGGATHCARY
                                                                                                                                                                     TTGTAGAAGTTGAGGAACCCAGTGATGGAACTATATTAGGGCGCTGGTGTGGTTCTGGTA
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                           801 NAARMGNTAYWSNTGYACNCCNWGNAAYTAYWSNGTNAAYATHMGNGARGARYTNAARYT
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--ATGCCACAATTCACAGAAGCTGTGAGTCCTTCAGTGCTAC
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                                                       TNCAYAAYIGYAAYGARTGYCARTGYGRINCCWASNAARGINACNAARAARTAYCAYGARG 923
                                                                                                                                                                    TCATACTTATCCAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGT 172
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Fatent No. 649568
GENERAL INFORMATION:
APPLICANT: Glibert, Teresa
APPLICANT: Bispard, Pair, Charles E.
APPLICANT: Bispard, Pail O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT APPLICATION NUMBER: US 09/304,216
PRIOR PLING DATE: 2000-05-03
PRIOR FLING DATE: 1999-01-10
PRIOR PLING DATE: 1999-11-10
PRIOR PLING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FLING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.0
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LOCATION: (1)...(1110)
OTHER INFORMATION: n = A,T,C or
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OTHER INFORMATION: degenerate
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GENERAL INFORMATION:
APPLICANT: Gilbert, Teresa
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul D.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
                                                                                                                            CURRENT PELICATION NUMBER: US/09/564,595D
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 09/304,216
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 2000-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 50.8
Matches 493; Conservative
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ORGANISM: Mus musculus
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LOCATION: (93)
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                                                    777 TGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAATAC 836
                                                                   837 CACGAGGICCITCAGIIGAGACC-----AAASACCGGIGICAGGGGAIIGCACAAA 887
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Search completed: November 26, 2003, 05:52:18 Job time : 81.0293 secs

Run

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TYPE: DNA
ORGANISM: Homo sapiens
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-131-600-4
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APPLICANT: BERKSSON, U1f

APPLICANT: BERKSSON, U1f

APPLICANT: AASE, Kaxin

APPLICANT: LEE, Xuri

APPLICANT: DEE, Xuri

APPLICANT: DINTEA, Marko

APPLICANT: DINTEA, Marko

APPLICANT: DESTINA, Annica

APPLICANT: DESTINA, Annica

APPLICANT: DESTINA, Annica

APPLICANT: BETSENCITZ, Christer

TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DI

TITLE OF INVENTION: THEREFOR, AND USES THEREOF

TITLE OF INVENTION: THEREFOR, AND USES THEREOF

TITLE OF INVENTION: THEREFOR, AND USES THEREOF

TITLE OF INVENTION: THEREFOR, AND USES THEREOF

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TITLE OF INVENTION: THEREFOR, AND USES THEREOF

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TITLE OF INVENTION: THEREFOR, AND USES THEREOF

TITLE OF INVENTION: THEREFOR, AND USES THEREOF

PRIOR FILING DATE: 1999-0-30

PRIOR PELICATION NUMBER: 60/113,002

PRIOR PELICATION NUMBER: 60/113,002

PRIOR PELING DATE: 1999-0-15

PRIOR PELING DATE: 1999-0-15

PRIOR PELING DATE: 1999-0-15

PRIOR PELING DATE: 1999-0-15

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SEQ ID NO 4

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Patent No. US20020164687A1
GENERAL INFORMATION:
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Length 1536;

DB 10;

Score 1535.6; Pred. No. 0;

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09 1081 CAGGATTTACAGTGCATTCTGAAAGAGACATCAAACAGAATTAGAACTTGCAACA 1140 DD 1081 CAGGATTTACAGTGCATTCTGAAAGAGACATCAACAGAATTAGAACTTGCAACA 1140  Qy 1141 GCTCTTTTGAGAGAGACCTAAAGACAAAAACAGAATTAGGAGTTGCAACA 1140  Qy 1201 TAAATGTTGTATTAAATAGATCACAGCTAGATTACAATTACAGTACATCACTCATCACTCATCACTCATCACTCATCACTCATCA	RESULT 2 US-10-11-600-4   Sequence 4. Application US/10131600   Publication No. US20030082670A1   APPLICANT: ERIKSSON, U1f   APPLICANT: RABE, Karin   APPLICANT: LEE, Xuri   APPLICANT: LEE, Xuri   APPLICANT: LEE, Xuri   APPLICANT: LOWERN, Annica APPLICANT: LITLAND CARTEN, ARNICA AND USES THERBOF   APPLICANT: UNTERLY, MARCO   APPLICANT: HIDAD, Kari   APPLICANT: UNTERLY, AND USES THERBOF   TITLE OF INVENTION: THERBER, AND USES THERBOF   TITLE OF INVENTION: THERBER, AND USES THERBOF   TITLE OF INVENTION: THERBER, AND USES THERBOF   TITLE OF INVENTION: THERBER, AND USES THERBOF   TITLE OF INVENTION: THERBER, AND USES THERBOF   TITLE OF INVENTION: THERBER, AND USES THERBOF   TITLE OF INVENTION: THERBER, AND USES THERBOF   TITLE OF INVENTION: THERBER, EN/10/131,600   CURRENT FILING DATE: 200-20-25   PRIOR FILING DATE: 1998-02-20   PRIOR APPLICATION NUMBER: 60/109,109   PRIOR APPLICATION NUMBER: 60/110,79   PRIOR APPLICATION NUMBER: 60/110,79   PRIOR PLING DATE: 1999-05-21   PRIOR PLING DATE: 1999-05-21   PRIOR PLING DATE: 1999-07-15   NUMBER OF SEQ ID NOS: 39   LENGTH: 1356   LENGTH: 1356   LENGTH: 1356   TYPE: DATA   CRANICAN: HOMO SADIENS   TYPE: DATA   CRANICAN: HOMO SADIENS   TYPE: DATA   CRANICAN: HOMO SADIENS
CGGGTAAATTCCAGTTTTCCAGCAACAAGAACAGAACGAGGTACAAGATCCTCAGCATG 60     CGGGTAAATTCCAGTTTTCCAGCAACAAGGAACAGAACGAGGTACAAGATCCTCAGCATG 60     CGGGTAAATTATTACTGATTTTCCAGCACAAGGAACGAGGTACAAGATCCTCAGCATG 60     CAGGAATTATTACTGATTTCCAGCAACAAGGAACGAGGTACAAGATTCCAAGATTCCAAGATT 120     CAGGAATTATTACTGATCAAAGAATTCACAGCCCAAGGTTACCTCAACATT 120     CAGGAATTATTACTGATCAAAGAATTCAAAGAACAAGATTCCAAGACTAACATT 120     CAGGAATTATTACTGATCAAAGAATTACTAAAGAAATTCACAGCCCAAGGTTTCCTCAAACTT 120     CAGGAATTATTACTGATCAAAAATTACTAAAGAAATTACTACAAGAAACTTACTAAACAAAAATTACTAAAAAAAA	481 ATANTGCTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATACTTGAACCAGAGA 540 481 ATANTGCTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATACTTGAACCAGAGA 540 541 GATGGCAGTTGGACTTAGAAGATCTATTAGGCAACTTTGGCAAGACTT 600 541 GATGGCAGTTGGACTTAGAAGATCTATAAGGCCAACTTGGCAACTTTTTGGCAAGGCTT 600 601 TTGTTTTTGGAAGAAAACTCATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTT 600 601 TTGTTTTTGGAAGAAAAACTCATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTT 600 601 TTGTTTTTGGAAGAAAAACTCAAAGAGCGAACTTGGCAACTTCTTGGCAAGGCTT 600 601 TTGTTTTTGGAAGAAAAACTCAGAGCGCAACTTGGCAACTTCTAACAGAGAGAG
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	Sequence 1, Application US/10178442
Similarity   100.0%;   Score 1535.6;   DB 14;   Length 1536;   Similarity   100.0%;   Pred. No. 0;   Indels   0;   Gaps   0;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;   Gaggrapartycactractacacacacacacacacacacacacacacacac	ATAATGCTATAGACTTAGAAGACCTTATTCGAAATCTTGAACCAGGG 540  ATAATGCTATAGACTTAGAAGACCTTATTATAGGCCAACTTCTTGGCAAGGCTT 600  GATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTCTTGGCAAGGCTT 600  GATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTCTTGGCAAGGCTT 600  TGTTTTTGGAAGAAAATCCAGAGTGGTGGAACTTCTTAACAGAGAGAAGATT 600  TTGTTTTTGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGAGAAGAT 660  TTGTTTTTGGAAGAAAATCCAGAGTGGTGGAACTTCTAACAGAGAGAG
Query Match Best Local Similarity 100 Matches 1536; Conservative Oy 1 CGGGTAAATTCCAGT Ob 61 AGAGAATTATTACTG Oy 61 AGAGAATTATTACTG Oy 121 ATCCAAGAAATACCG Oy 121 ATCCAAGAAATACGG Oy 181 AACTTACGTTTGATG Oy 241 ATTTGTAGAAGTTG Oy 241 ATTTGTAGAAGTTG Oy 301 GTACTGATTGAGGAGTTG Oy 301 GTACTGATACCAGGAA Oy 301 GTACTGATACCAGGAA Oy 301 ATTTGTAGAAGTTCCTT Ob 301 ATTTGTAGAAGTTCCTT Oy 361 ATGAATATTTCCTT Oy 361 ATGAATATTTCCTT Oy 361 ATGAATATTTCCTT Oy 421 TCACAGAAGCTGTGA Oy 421 TCACAGAAGCTGTGA Oy 421 TCACAGAAGCTGTGA Oy 481 ATAATGCTATAAACTC	481 481 541 601 601 721 721 721 721 721 721 721 72

	RESULT 4 US-09-978-295A-487 US-09-978-295A-487  Squence 487, Application US/09978295A  Patent No. US20020156006A1  GENERAL INFORMATION:  APPLICANT: Baker Kevin P.  APPLICANT: Botstein, David  APPLICANT: Betton, Dan  APPLICANT: Ferrara, Napoleon  APPLICANT: Ferrara, Napoleon  APPLICANT: Ferrara, Napoleon  APPLICANT: Filan  APPLICANT: Gao, Wei-Qiang  APPLICANT: Gao, Wei-Qiang  APPLICANT: Georetser, Elen  APPLICANT: Gao, Wei-Qiang  APPLICANT: Gao, Wei-Qiang  APPLICANT: Gao, Wei-Qiang  APPLICANT: Gar, Mei-Qiang  APPLICANT: Gar, Mei-Qiang	APPLICANT: Goddard, Audrey, APPLICANT: Goddard, Audrey, APPLICANT: Goddowski, Paul J. APPLICANT: Grimaldi, J. Christopher APPLICANT: Gurney, Austin L. APPLICANT: Hillan, Renneth J. APPLICANT: Hillan, Renneth J. APPLICANT: Napier, Mary A. APPLICANT: Napier, Mary A. APPLICANT: Paoni, Nicholas F. APPLICANT: Roy, Margaret Ann APPLICANT: Shelton, David L. APPLICANT: Tumas, Daniel APPLICANT: Tumas, Daniel APPLICANT: Pumas, Daniel APPLICANT: Williams, P. Mickey	### ### ##############################
64 GAATTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATC 123  401 GAATTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATC 160  124 CAAGAAATTACTGTGTATGGAATTACTACAGCCCAAGGTTTCCTCATACTTATC 460  124 CAAGAAATTACGGTTTGGAGATTAGTAGCAGTAGGAAAATGTATGGATACAAC 183  461 CAAGAAATTACGGTTTGGAGATTAGTAGCAGTAGAGAAATGTATGGATACAAC 520  184 TTACGTTTGATGAAAGATTTGGAGATTAGTAGCAGTAGAGAAATGTATGGATACAAC 520  244 TTGTAGAAGTTGAGGAATTAGGAGTTGGAAGATAGAATAGATT 243  251 TTACGTTTGATGAAAAGATTTGGAGATTAGAAGAATAGAATAGATT 580  247 TTGTAGAAGTTGAGGAACCCAGTGATGGAACTATATAGGAGAAATGTATGGATAGAT 580  304 CTGTACCAGGAAAACGGAATTTCTAAAGGAATTAGGAGTAGGATTGTATCTGATG 363  401 CTGTACCAGGAAAACGGAATTTCTAAAGGAAATTAGGATAAGATTTGTATCTGATG 700  364 AATATTTCCTTCTGGAACCAGGGTTCTGCATCCACTACAATTGTATTGTATCTGATG 700  364 AATATTTTCCTTCTGAACCAGGGTTCTGCATCCACTACAATTGTATTGTATCTGATG 700  424 CAGAAGCTGTGAACCAGGGTTCTGCATCCACTACAATTGTATTGTATTGTATCTAATA 830  426 CAGAAGCTGTGAACCAGGGTTCTGCATCCACTACAATTGTATTGTATTCTAATA 830  461 CAGAAGCTGTGAACTACAGTGAACCACTACACTTGTCATGCCACAATTCA 760  424 CAGAAGCTGTGAACTACACTACACACTTGCCATAAATA 820  461 CAGAAGCTGAAGTGTAACCACTCACACTTGCCATAAATA 820	84 ATGCTATAACTGCCT 21 ATGCTATAACTGCCT 44 GGCAGTTGGACTTAG 81 GGCAGTTGGAAAA 04 TTTTTGGAAGAAAA 11	724 CCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTCGGAACTGTGCCTGTTGTC 783  1061 CCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTCGGAACTGTGCCTGTTGTC 1120  784 TCCACAATTGCAATGAATGTCTCCCAAGCAAAGTTACTAAAAAATCCCAGAGG 843  1121 TCCACAATTGCAATGAATGTCTCCCAAGCAAAGTTACTAAAAAATACCACGAGG 1180  844 TCCTTCAGTTGAATGAATGTCTCCCAAGCAAAGATACCACCAGAGGG 1180  847 TCCTTCAGTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA	

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Pred. No. 0;
1; Mismatches
DR APPLICATION NUMBER: 60/085689

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DR FILING DATE: 1998-05-15

DR APPLICATION NUMBER: 60/085580

DR APPLICATION NUMBER: 60/085573

DR FILING DATE: 1998-05-15

DR APPLICATION NUMBER: 60/08573

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Garber, Hanspeter Gerritsen, Mary B. Goddard, Audrey Godowski, Paul J. Grimaldi, J. Christopher Hillan, Kenneth J Kljavin, Ivar J. Kno, Sophia S. Napier, Mary A. Pan, James; Sequence 487, Application US/09978697; Patent No. US20020169284A1; GENERAL INFORMATION: APPLICANT: Ashkenazi, Avi APPLICANT: Baker Kevin P. APPLICANT: Botstein, David APPLICANT: Bosnoyers, Luc APPLICANT: Eaton, Dan APPLICANT: Ferrara, Napoleon APPLICANT: Forey Sherman APPLICANT: Fong, Sherman APPLICANT: Gao, Wei-Qiang

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PRIOR APPLICATION NUMBER: 60/081049
PRIOR PILING DATE: 1998-04-08
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PRIOR PELICATION NUMBER: 60/081049
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APPLICATION NUMBER: 60/084639
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APPLICATION NUMBER: 60/084441
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APPLICATION UNMBER: 60/080328
FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080333
      Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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                                        TTTTTGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTAT
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; Patent No. US20020177553A1
; GENERAL INFORMATION:
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R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/084598

R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/084600

R APPLICATION NUMBER: 60/084627

R APPLICATION NUMBER: 60/084637

R FILING DATE: 1998-05-07

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R APPLICATION NUMBER: 60/085323

R FILING DATE: 1998-05-15

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R FILING DATE: 1998-05-15
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R APPLICATION NUMBER: 60/085573
R FILING DATE: 1998-05-15
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                      R APPLICATION NUMBER: 60/079786
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R APPLICATION NUMBER: 60/079923
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DR APPLICATION NUMBER: 60/082796

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R FILING DATE: 1998-04-28

DR APPLICATION NUMBER: 60/08332

R FILING DATE: 1998-04-28

DR APPLICATION NUMBER: 60/08392

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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
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APPLICATION NUMBER: 60/079728
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Filvaroff, Ellen
Fong, Sherman
Ashkenazi, Avi
Baker Kevin P.
Botstein, David
Desnoyers, Luc
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Gao, Wei-Qiang
   APPLICANT:
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	304 CTGTACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGTG 363 	364 AATATTTTCCTTCTGAACCAGGTTCTGCATCCACTACAACATTGTCATGCACAATTCA 423 	424 CAGAAGCIGIGAGICCTICAGIGCTACCCCCTICAGCTITGCCACIGGACCIGCITAAIA 483 	484 AIGCTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGT 543 	544 GGCAGTIGGACTIAGAAGAICTAIAIAGGCCAACTIGGCAACTICTIGGCAAGGCTITIG 603	604 TTTTTGGAAGAAAATCCAGAGTGGTCGATCTGAACCTTCTAACAGAGGGGGTAAGATTAT 663 	664 ACAGCIGCACACCICGIAACTICTCAGIGTCCAIAAGGGAAGAACTAAAGAGAACGATA 723 	724 CCATTITCTGGCCAGGITGTCTCCTGGTTAAACGCTGTGGGAACTGTGCCTGTTGTC 783 1087 CCATTITCTGGCCAGGITGTCTCCTGGTTAAACGCTGTGGGAACTGTGCCTGTTGTC 1146	784 TCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACCACGAGG 843 	844 TCCTTCAGTTGAGACCAAASACGGTGTCAGGGGATTGCACAAATCACTCACCGACGTGG 903	904 CCCTGGAGCACCATGAGGAGTGTGACTGTGTGCAGAGGAAGCACAGGAGGATAGCCGC 963	964 ATCACCACACACACTCTTGCCCAGACTGTGCAGTGCAGT	1024 CGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAG 1083 1387 CGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAG 1446	1084 GAITTACAGTGCAITCTGAAAGAGAGACAICAAACAGAAITAGGAGTTGTGCAACAGCT 1143 	CTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAA	AIGTIGTATTAAATAAATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGC	1264 TGGGTTCTGTATTTCATTTCGATACGGCTTAGGCTAATGTCACTACAGGAAAAAA	
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PRIOR APPLICATION NUMBER: 60/083554 PRIOR FILING DATE: 1998-04-29				PRIOR APPLICATION NUMBER: 60/08441  PRIOR FILING DATE: 1998-05-06  PRIOR FILING DATE: 60/084637  PRIOR FILING DATE: 1998-05-07	<pre>prior Application NUMBER: 60/084639 prior Filling DaTE: 1998-05-07 prior Application NUMBER: 60/084640 prior PILING DATE: 1998-05-07</pre>	prior Application Winder: 60/084598 prior Filing Date: 1998-05-07 prior Application Winder: 60/084600 prior Piling Date: 1998-05-07		PRIOR PRIOR PRIOR	PRIOR PRIOR PRIOR		PRIOR PRIOR PRIOR	PRIOR APPLICATION NUMBER: 60/0855/3 PRIOR FILING DATE: 1998-05-15 PRIOR PILING DATE: 1998-05-15 PRIOR PILING DATE: 1998-05-15	PRIOR AFFLICATION NUMBER: 00/00003/ Query Match 99.8%; Score 1532.6; DB 10; Length 2849; Best Local Similarity 99.9%; Pred, No. 0; Match 1533. Concornative in Mismatches 0. Indels 0.	MACCHES 1532; CONSELVATIVE I, MISMACCHES V, INCEIB V, GALS 4 GTAAATTCCAGCAACAACAACAACGAACGAACGAAGAACAAGAACGAACGAAGAA		Qy 124 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAAC 183 Db 487 CAAGAAATACGGTCTTGGTATGGAGTTAGTAGCAGTAGAGGAAAATGTATGGATACAAC 546	TTACGTTTGAAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATT 	

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A AFFLICATION NOMBER: 60/079505

R APPLICATION NUMBER: 60/079664

RR PILING DATE: 1998-03-26

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RR APPLICATION NUMBER: 60/07963

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R APPLICATION NUMBER: 60/081049
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APPLING DATE: 1998-03-25
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APPLICATION NUMBER: 60/081955
FILING DATE: 1998-04-15
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              APPLICATION NUMBER: 60/078886
FILING DATE: 1998-03-20
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APPLICATION NUMBER: 60/078910
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APPLICATION NUMBER: 60/081229
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APPLICATION NUMBER: 60/082804
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 1807 ACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAAT 1866
1687 CTGTGCAAGTGAGCACCTGATTCCGTTGCCTTAACTCTAAAGCTCCATGTCCTGGG 1746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
ITTLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITTLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC63
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT FILING DATE: 2001-00-30
PRIOR PILING DATE: 2001-00-30
PRIOR APPLICATION NUMBER: 60/06226
PRIOR APPLICATION NUMBER: 60/064249
PRIOR APPLICATION NUMBER: 60/064249
PRIOR APPLICATION NUMBER: 60/066364
PRIOR APPLICATION NUMBER: 60/066364
PRIOR PILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/07631
PRIOR PILING DATE: 1998-03-10
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PRIOR PILING DATE: 1998-03-11
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                                                                                                                                                                           TAAACTTGTGTCATGCTGATAGGACAGACTGGA 1536
                                                                                                                                                                                                 Sequence 487, Application US/09999832A Publication No. US20020192706A1 GENERAL INFORMATION:
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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APPLICATION NUMBER: 60/078004
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Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Kuo, Sophia S.
Napier, Mary A.
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APPLICANT: Baker Kevin P
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R APPLICATION NUMBER: 60/079656

R FILING DATE: 1998-03-26

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R APPLICATION NUMBER: 60/079664

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R APPLICATION NUMBER: 60/079663

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R APPLICATION NUMBER: 60/079920
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R APPLICATION NUMBER: 60/077641

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R APPLICATION NUMBER: 60/07791

R FILING DATE: 1998-03-20

R APPLICATION NUMBER: 60/07886

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R APPLICATION NUMBER: 60/078936

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R APPLICATION NUMBER: 60/080333
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APPLICATION NUMBER: 60/081195
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                   APPLICATION NUMBER: 60/062250
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APPLICATION NUMBER: 60/077632
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1387 CGTATGCGTTATCTCCATCCTTAATCTCGGTTGTTTGAAGGACCTTTCATCTTCAGG 1446
                                                                                                                                                                                                     1204 AIGITGIATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGC 1263
                                                                                                                                                                                                                                                                                                                                                                           1264 TGGGTTCTGTATTTCAGTTCTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAA 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1687 CTGTGCAAGTGAGCACCTCATTCCGTTGCCTTGCTTAACTCTAAAGCTCCATGTCCTGGG 1746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1444 ACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAAT 1503
                                                                                                     1447 GATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCT 1506
                                                                                                                                                                                                                                                                                                     1567 ATGTTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGC
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                                                                                                                                                             GATITIACAGIGCATITCIGAAAGAGGAGACATCAAACAGAATIAGGAGTIGIGCAACAGCI
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Gerritsen, Mary E.
Geddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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US-09-978-189-487
Sequence 487, Application US/09978189
Publication No. US20030004102A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
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Pan, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Botstein, David
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Eaton, Dan
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RR APLICATION NUMBER: 60/081817
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RR FILING DATE: 1998-04-15
RR APPLICATION NUMBER: 60/081952
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RR APPLICATION NUMBER: 60/08256
RR APPLICATION NUMBER: 60/08269
RR FILING DATE: 1998-04-21
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426 486 183 546 243 TITITGGAAGAAATCCAGAGTGGTGGTCTTGTACTTCTAACAGAGGAGGAAGATTAT 1026 909 303 999 363 CTGTACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATG 726 423 786 CAGAAGCTGTGAGTCCTTCAGTGCTACCCCTTCAGCTTTGCCACTGGACCTGCTTAATA 483 846 543 663 783 906 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG 603 907 GGCAGTIGGACTIAGAAGAICTATATAGGCCAACTIGGCAACTICTIGGCAAGGCTTTIG 966 63 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAAC CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAAGAAAATGTATGGATACAAC CAGAAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATA GAATTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCCAAGGTTTCCTCATACTTATC GAATTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATC TTGTAGAAGTTGAGGAACCCAGTGATGGAACTATATAGGGCGCTGGTGTGGTTCTGGTA ridradaadridaddaacccagrearddaacrarrinadddccrecrecrecriccrecra ATGCTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGT ATGCTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGAT GTAAATTCCAGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGA TTACGTTTGATGAAGATTTGGGCTTGAAGACCCCAGAAGATGACATATGCAAGTATGATT TTACGTTTGATGAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATT CTGTACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATG TITITGGAAGAAAATCCAAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTAT ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA CCATTITCTGGCCAGGIIGICICCCGGTTAAACGCTGTGGTGGGAACTGTGCCTGTTGTC Gaps Length 2849; ; 0 0; Indels DB 11; 99.8%; Score 1532.6; 99.9%; Pred. No. 0; tive 1; Mismatches PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR APPLICATION NUMBER: 60/085582
PRIOR PLING DATE: 1998-05-13
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PRIOR PELING DATE: 1998-05-15
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PRIOR PELING DATE: 1998-05-15 Best Local Similarity 99.9 Matches 1532; Conservative . 496 4 64 427 124 487 184 547 244 607 304 667 364 727 424 787 484 847 544 604 664 1027 724 Query Match qq 셤 g g g 8 8 ద 셤 В ò ઠે à à ð ò ₽ à 셤 à 셤 ò à 셤 ð

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              APPLICANT: Gurnella, Kenneth J
APPLICANT: Gurnella, Kenneth J
APPLICANT: Hillan, Kenneth J
APPLICANT: Kijavin, Ivar J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Koo, Sophia S.
APPLICANT: Pan, James;
APPLICANT: Pan, James;
APPLICANT: Pan, James;
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timcthy A.
APPLICANT: Stewart, Timcthy A.
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucl
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC22
CURRENT FILING DATE: 2001-10-16
NUBBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrapper or Palm
SEQ ID NO 487
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    Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: unknown base US-09-978-608A-487
Grimaldi, J. Christ
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: unsure
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                                              TCCACAATTGCAATGTCAATGTCTCCCAAGCAAAGTTACTAAAAAATACCACGAGG
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Publication No. US20030045462A1

GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Bakar Kevin P.
APPLICANT: Borstein, David
APPLICANT: Berstein, David
APPLICANT: Bersovers, Luc
APPLICANT: Ferrara, Napoleon
APPLICANT: Ferrara, Napoleon
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gacher, Hanspeter
APPLICANT: Gacher, Hanspeter
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
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US-09-978-608A-487
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630P1C15
FULE REFERENCE: P2630P1C15
CURRENT APPLICATION NUMBER: US/09/978,585A
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624
                                                                                                                                                                                                                                                                                                                                                                                                               - See File Wrapper or Palm
                                                                                                                                       Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J.
KLjavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: unknown base US-09-978-585A-487
                                                                                                                                                                                                                               Pan, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
                                                                                                                                                                                                                                                                                                          Williams, P. Mickey Wood, William I.
                                                                                                                                                                                                                                                                                  Stewart, Timothy A.
                                                 Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
                                                                                                                 Gerritsen, Mary E.
                                                                                                     Gerber, Hanspeter
Baker Kevin P.
Botstein, David
Desnoyers, Luc
                                                                                                                               Goddard, Audrey
                                                                                                                                                                                                                                                                                              Tumas, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: unsure
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 GGCAGTIGGACTIAGAAGAICIATATAGGCCAACTIGGCAACTICTIGGCAAGGCTTTIG 966
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                            TITITIGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTAT
                                             ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAAGAACCGATA
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Sequence 487, Application US/09978585A Publication No. US20030049633A1 GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi

RESULT 10 US-09-978-585A-487

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                         1504 TARACTIGIGICALGCIGAIAGGACAGACIGGA
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Goddwski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
Pan, James;
Pani, James;
                                                                                                                                                                                                              ; Sequence 487, Application US/09978191A; Publication No. US20030050239A1; GENERAL INFORMATION;
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R APPLICATION NUMBER: 60/078919

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Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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APPLICANT: Baker Kevin D.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
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Filvaroff, Ellen
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PRIOR APPLICATION NUMBER: 60/079663
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367 GTABATTCCAGTTTTCCAGCAACAGAACAGAACGGAGTACAAGATCCTCAGCATGAGA 426 64 GAATTATTACTGTGTCTACTAATGGAAGTATTCACAGGCCAAGGTTTCCTCATACTTATC 123 4 GTAAATTCCAGTTTTCCAGCAACAAGAACAGAACGGAGTACAAGATCCTCAGCATGAGA Gaps Query Match 99.8%; Score 1532.6; DB 11; Length 2849; Best Local Similarity 99.9%; Pred. No. 0; Matches 1532; Conservative 1; Mismatches 0; Indels 0; R APPLICATION NUMBER: 60/084441

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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Roy, Margaret Ann
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Gerber, Hanspeter
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Botstein, David
Desnoyers, Luc
Eaton, Dan
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PRIOR APPLICATION NUMBER: 60/085579
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PRIOR APPLICATION NUMBER: 60/08573
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R APPLICATION NUMBER: 60/081817

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R FILING DATE: 1998-04-15

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PRIOR APPLICATION NUMBER: 60/084598  PRIOR FILING DATE: 1998-05-07  PRIOR PILING DATE: 1998-05-07  PRIOR PLILING DATE: 1998-05-07  PRIOR APPLICATION NUMBER: 60/084643  PRIOR APPLICATION NUMBER: 60/084643  PRIOR APPLICATION NUMBER: 60/08539  PRIOR FILING DATE: 1998-05-07  PRIOR APPLICATION NUMBER: 60/08539  PRIOR FILING DATE: 1998-05-13  PRIOR APPLICATION NUMBER: 60/08532  PRIOR APPLICATION NUMBER: 60/08532  PRIOR PILING DATE: 1998-05-13  PRIOR APPLICATION NUMBER: 60/08570  PRIOR FILING DATE: 1998-05-15  PRIOR APPLICATION NUMBER: 60/08570  PRIOR FILING DATE: 1998-05-15  PRIOR PILING DATE: 1998-05-15	Query Match Best Local Similarity 99.8%; Score 1532.6; DB 11; Length 2849; Best Local Similarity 99.9%; Pred. No. 0; Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Qy 4 GTAAATTCCAGTTTTCCAGCAACAAGGAACAGAACAGAA		ACAAC CCAAC CGATT	244 TICTAGAACTTGAGGAACCCAGTGAACTATATAGGGGCTGGTGTGTTCTGGTA  607 TICTAGAAGTTGAGGAACCCAGTGAACGAACTATATAGGGCGCTGGTTCTGGTA  304 CTGTACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAGATA	Db   667 CTGTACCAGGAAACAGATTTCTAAAGGAAATCAATTAGATAAGATTTGTTGTTGTGTG   726     Oy   364 AATATTTCCTTCTGAACCAGGGTTCTGCATCACTACAATTCATGCACAATTCA   423     Db   727 AATATTTTCTTCTGAACCAGGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCA   786     Oy   424 CAGAAGCTGTGAGTCCTTCAGGGTTCTCAGCTTTGCCACTGGAACTTAATA   483     Oy   624 CAGAAGCTGTGAGTCCTTCAGGTTCTCAGCTTTGCCACTGGACCTGCTTAATA   636     Ob   787 CAGAAGCTGTGAGTCCTTCAGTGCTACCCCTTCAGCTTTGCCACTGGACCTGCTTAATA   846     Ob   787 CAGAAGCTGTGAGTCCTTCAGTGCTACCCCTTCAGCTTTGCCACTGGACCTGCTTAATA   846     Ob   787 CAGAAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATA   846     Ox   787 CAGAAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATA   846     Ox   787 CAGAAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATA   846     Ox   787 CAGAAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATA     Ox   787 CAGAAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATA     Ox   787 CAGAAGCTGTGAGTCCTTCAGTGCTTCAGCTTCAGAATA     Ox   787 CAGAAGCTGTGAGTCCTTCAGTGCTTCAGCTTCAGAATA     Ox   787 CAGAAGCTGTGAGTCCTTCAGTGCTTCAGCTTCAGAATA     Ox   787 CAGAAGCTGTGAGTCTTCAGTGCTTCAGCTTCAGAATA     Ox   787 CAGAAGCTGTGAGTCTTCAGTGCTTCAGTAGTAGTAGTTAGT	QY         484 AIGCIAIDACTGCTTIAGTACCTTIGGAAGACCTTATTCGAIATCTTIGAACCAGAGAGAT 543           DD         847 AIGCIAIDACTGCTTIAGTACCTTIGGAAGACCTTATTCGAIATCTTIGAACCAGAGAAT 906           QY         544 GGCAGTIGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTTGGCAACTTTG 603           DD         907 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTTGGCAAGGCTTTTG 603           DD         907 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTTGGCAAGGCTTTTG 966

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APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Grimaldi, J. Christopher
APPLICANT: Hillan, Keneth J
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APPLICANT: Kljavin, Ivart J.
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APPLICANT: Paoni, Nicholas F.
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William I.
TITLE OF INVENTION: Screed and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: Park A.
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CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
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PRIOR PELING DATE: 2001-10-24
PRIOR FILING DATE: 1097-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-11-13
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R APPLICATION NUMBER: 60/079663
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Filvaroff, Ellen
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Gerritsen, Mary E.
Goddard, Audrey
     Botstein, David
Desnoyers, Luc
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304 CTGTACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATG 363 667 CTGTACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATG 726 364 AATATTTCCTTCTGAACCAGGGTTCTGCATCCACACATTGTCATTTCCTTCTGAACCAGGGTTCTGCATTCACACACA		4 ACACTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACGGATA	4 H-H D-D 4-	3.89 4.4.70 7.00 7.00 7.00	CTTTTGAGAGGGCCTAAAGGACAGGGAAAAGGTCTTCAATCGTGGAAAGAAA	1264 IGGGTTCTGTATTTCAGTTCTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAA 1323 1627 TGGGTTCTGTATTTCAGTTCTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAA 1686 1324 CTGTGCAAGTGAGCACCTGATTCCGTTGCTTAACTCTTAAAGTCCATGTCCATGTTCTGGG 1383
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PRIOR APPLICATION NUMBER: 60/083558  PRIOR FILING DATE: 1998-04-29  PRIOR FILING DATE: 1998-04-29  PRIOR PILING DATE: 1998-04-29  PRIOR PILING DATE: 1998-04-29  PRIOR FILING DATE: 1999-04-30  PRIOR FILING DATE: 1999-04-30  PRIOR FILING DATE: 1998-04-30  PRIOR PILING DATE: 1998-04-30  PRIOR FILING DATE: 1998-05-05  PRIOR FILING DATE: 1998-05-05  PRIOR FILING DATE: 1998-05-06  PRIOR APPLICATION NUMBER: 60/08441  PRIOR FILING DATE: 1998-05-06  PRIOR APPLICATION NUMBER: 60/08441  PRIOR FILING DATE: 1998-05-06  PRIOR APPLICATION NUMBER: 60/08441	PRIOR FILING DATE: 1998-05-07 PRIOR FILING DATE: 1998-05-07 PRIOR FILING DATE: 1998-05-07 PRIOR FILING DATE: 1998-05-07 PRIOR PILING DATE: 1998-05-07 PRIOR APPLICATION NUMBER: 60/084640 PRIOR FILING DATE: 1998-05-07 PRIOR PILING DATE: 1998-05-07 PRIOR APPLICATION NUMBER: 60/084600 PRIOR APPLICATION NUMBER: 60/084600 PRIOR APPLICATION NUMBER: 60/084600 PRIOR FILING DATE: 1998-05-07 PRIOR APPLICATION NUMBER: 60/084627		PRIOR APPLICATION NUMBER: 60/085700  PRIOR FILING DATE: 1998-05-15  PRIOR APPLICATION NUMBER: 60/085699  PRIOR APPLICATION NUMBER: 60/085579  PRIOR APPLICATION NUMBER: 60/085580  PRIOR APPLICATION NUMBER: 60/085580  PRIOR FILING DATE: 1998-05-15  PRIOR FILING DATE: 1998-05-15  PRIOR FILING DATE: 1998-05-15  PRIOR PLICATION NUMBER: 60/085573  PRIOR PLICATION NUMBER: 60/085774  PRIOR APPLICATION NUMBER: 60/085774	AFFLICATION NUMBER: 00/085/04  FILING DATE: 1998-05-15  APPLICATION NUMBER: 60/085697  APPLICATION NUMBER: 60/085697  APPLICATION NUMBER: 60/085697  Social Similarity 99.9%; Pred. No. 0; O; Indels 0; Gaps  4 GTAAATTCCAGTTTTCCAGCAACAAGGAACAGAACGGAGTACACACCAGCATGAGA 63	GAATTATTACTGTGTCTACTAATGGAAGTATTCACAGGCGGAGGTTCCTCAGGGAATTATTACTGTGTCTAATGGAAGTATTCACAGGCCCAAGGTTTCCTCATGGAAGTATTCACAGGCCCAAGGTTTCCTCATGGAAATTAGTAACAGGAAATAGGAAAATAGGAGAAAATGGAGAAAATGGAGAAAATAGTAG	ATGATT ATGATT ATGGTA

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1747 CCTAAAATCGFATAAAATCTGGATTTTTTTTTTTTTTTGCTCATATTCACATATGTAA 1806
                                                                                                                                                                                               1807 ACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAAT 1866
                                                                                                                                                    1444 ACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAAT 1503
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APPLICANT: Thus, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC12
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CURRENT PEPLICATION NUMBER: US/09/981,915A
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: US/918585
PRIOR FILING DATE: 12001-07-30
PRIOR FILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-11-13
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PRIOR PELING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR PILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/076364
PRIOR PILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR PILING DATE: 1998-03-10
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PRIOR APPLICATION NUMBER: 60/07886
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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8-09-091-915A-487
7 Sequence 487, Application US/09981915A
7 Publication No. US20030054986A1
7 GENERAL INPORMATION:
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Filvaroff, Ellen
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Shelton, David L.
Stewart, Timothy A.
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Paoni, Nicholas F.
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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PRIOR PLING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR APLICATION NUMBER: 60/081819
PRIOR PILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
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RRIOR APPLICATION NUMBER: 60/082704
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
RRIOR RILING DATE: 1998-04-22
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R APPLICATION NUMBER: 60/079663

R APPLICATION NUMBER: 60/079728

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R APPLICATION NUMBER: 60/079786

R APPLICATION NUMBER: 60/079786

R APPLICATION NUMBER: 60/079920

R FILING DATE: 1998-03-27

R APPLICATION NUMBER: 60/079920

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R APPLICATION NUMBER: 60/080327
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RR FILING DATE: 1998-04-01
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APPLICATION UNDERS: 60/081049
FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081071
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APPLICATION UNMBER: 60/081203
APPLICATION UNMBER: 60/081229
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APPLICATION UNMBER: 60/080107
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APPLICATION NUMBER: 60/080165
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APPLICATION NUMBER: 60/081195
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli
di	1 PCT-US99-22668-4 2 PCT-US99-22668-4 21 US-09-410-349A-4 35 US-09-852-209-4
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                                                                 100.0%; Score 1535.6;
llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
; TYPE: DNA
; ORGANISM: Homo sapiens
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APPLICANT: HELSINKI UNIVERSITY LICENSING LTD.
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,
CURRENT PRIDICATION NUMBER: PCT/US99/22668B
CURRENT FILING DATE: 1999-09-30
BARLIER APPLICATION NUMBER: 60/102,461
EARLIER PILING DATE: 1998-10-30
EARLIER PILING DATE: 1998-11-12
EARLIER PILING DATE: 1998-11-3
EARLIER PILING DATE: 1998-12-3
EARLIER FILING DATE: 1998-12-3
EARLIER FILING DATE: 1999-05-21
EARLIER FILING DATE: 1999-05-21
EARLIER FILING DATE: 1999-05-21
EARLIER FILING DATE: 1999-07-15
NUMBER: 06/144,022
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Pred. No. 0;
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Oy 1081 CAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACA 1140	Qy 1141 GCTCTTTGAGAGGAGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAAAA 1200	OY 1201 TAAATGTTGTATTAAATAGATCACCAGGTAGTTTCAGAGTTACCATGTACGTATTCCACT 1260	OY 1261 AGCTGGGTTCTGTATTTCAGTTCTTTCGATAGGGGTAAGGGTAATGTCAGTACAGGAAAA 1320 	Qy 1321 AAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTAACTCTAAAGCTCCATGTCT 1380	Oy 1381 GGGCCTAAAATCCTATAAATCTGGATTTTTTTTTTTTTT	QY 1441 TAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAGGAACTATGTTGCTATG 1500 	QY 1501 AATTAAACTTGTGTCATGCTGATAGGACAGACTGGA 1536 	RESULT 3 US-09-410-349A-4 ; Sequence 4, Application US/09410349A	; GENERAL INFORMATION: ; APPLICANT: ERIKESON, Ulf ; APPLICANT: ASS, Karin ; APPLICANT: LEE, Xuri	; APPLICANT: PONTEN, Annica ; APPLICANT: UUTELA, Marko ; APPLICANT: ALITALO, Kari ; APPLICANT: ALITALO, Arri	; APPLICANT: HELDIN, Carl-Henrik ; APPLICANT: BETGHOLTZ, Christer ; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING ; TITLE OF INVENTION: THEREPOR, AND USES THEREOF	; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740 ; CURRENT APPLICATION NUMBER: US/09/410,349A ; CURRENT PILLIG DATE: 1999-09-30 ; PRIOR APPLICATION NUMBER: 60/108,109	; PRIOR FILING DATE: 1998-11-12; PRIOR APPLICATION NUMBER: 60/110,749; PRIOR APPLICATION TOWNER: 60/113,002; PRIOR APPLICATION NUMBER: 60/113,002	; PRIOR FILING DATE: 1998-12-18 ; PRIOR APPLICATION NUMBER: 60/135,426 ; PRIOR APPLICATION TOWER: 60/135,426 ; PRIOR APPLICATION TUMBER: 60/14,022	; PRIOR FILING DATE: 1999-07-15; NUMBER OF SEQ ID NOS: 39 ; SOFTWARE: Patentin Ver. 2.0 ; SEO ID NO 4	; LENGTH: 1536 ; TYPE: DNA ; ORGALIN: Homo sapiens US-09-410-349A-4	Query Match 100.0%; Score 1535.6; DB 21; Length 1536; Best Local Similarity 100.0%; Pred. No. 0; Matches 1536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1021 GAACGTATGCCTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTT 1080
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                                                                                                     61 AGAGAATTATTACTGTGTCTACTAATAGAAGTATTCACAAGGTTTCCTCATACTT 120
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APPLICANT: HELDIN, CARI-Henrik
APPLICANT: BETSHOLTZ, Christer
ITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,
ITLE OF INVENTION: THEREFOR, AND USES THEREOF
FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
CURRENT APPLICATION NUMBER: US/09/852,209
CURRENT APPLICATION NUMBER: 09/410,349
FRIOR PILING DATE: 1999-09-30
PRIOR PILING DATE: 1998-12-03
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR APPLICATION NUMBER: 60/1135,426
PRIOR APPLICATION NUMBER: 60/1135,426
PRIOR APPLICATION NUMBER: 60/114,022
PRIOR APPLICATION NUMBER: 60/144,022
PRIOR APPLICATION NUMBER: 60/144,022
PRIOR PILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 60/144,022
PRIOR PILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATCHILIN VET: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: AASE, Karin
APPLICANT: LEE, Xuri
APPLICANT: PONTEN, Annica
APPLICANT: UUTELA, Marko
APPLICANT: ALITALO, Kari
APPLICANT: OESTWAN, Arne
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ORGANISM: Homo sapiens
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      CGGGTAAATTCCAGTTTTCCAGCAACAAGAACAGAACGGGGTACAAGATCCTCAGCATG
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| GENERAL INFORMATION: |
| APPLICANT: ERIKSON, U1f |
| APPLICANT: LEE, Kuri |
| APPLICANT: LEE, Kuri |
| APPLICANT: UUTELA, Marko |
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| FILE OF INVENTION NUMBER: US/09/852,209A |
| PRIOR FILING DATE: 1999-09-30 |
| PRIOR FILING DATE: 1999-05-21 |
| PRIOR FILING DATE: 1999-07-15 |
| NUMBER OF SEQ ID NOS: 39 |
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                                                                                                                                                                                                AGCTGGGTTCTGTATTTCAGTTCTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAA 1320
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APPLICANT: HELDIN, CAIL-Henrik
APPLICANT: BETSHOLTZ, Christer
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,
TITLE OF INVENTION: THEREPOR, AND USES THEREOF
TITLE OF INVENTION: THEREPOR, AND USES THEREOF
FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
CURRENT PRIOR APPLICATION NUMBER: US/09/410,349
FRIOR APPLICATION NUMBER: US/09/410,349
PRIOR APPLICATION NUMBER: 60/108,109
PRIOR APPLICATION NUMBER: 60/110,749
FRIOR PRIOR PRICE 1998-11-12
PRIOR FILING DATE: 1998-12-03
PRIOR FILING DATE: 1998-12-03
PRIOR FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 39
SEGFWARE PREDIT VOIL VET: 2.0
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GENERAL INFORMATION:
APPLICANT: BRIKSSON, UIF
APPLICANT: AASE, Karin
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UUTELA, Marko
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OESTMAN, Arne
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LEE, Xuri
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US-10-131-600-4
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1001 CAGGATTPACAGGGCCTAAAGGGACATCAACAAATTAGGACTATTGCAACAATTAGGACAATTAGGACAATTAGGACAATTAGGACAATTAGGACAAATTAGGACAAATTAGGACAAATTAGGACAAATTAGGACAAATTAGGACAAATTAGGACAAATTAGGACAAATTAGGACAAATTAGCAAAATTAGAATTAGAAATTAGAATTA	DENGTH: 1536 TYPE: DNA TYP

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                                                                                                                                                                            AGCTGGGTTCTGTATTTCAGTTCTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAA
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99.8%; Score 1532.6; DB 16; Length 2825;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1532; Conservative 1; Mismatches 0; Indels 0; 0
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GENERAL INFORMATION:
APPLICANT: Ferrara, Napoleone
APPLICANT: Kno, Sophia S.
TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMPI
FILE REFERENCE: P1122P1
CURRENT APPLICATION UNBER: US/09/184,216
CURRENT APPLICATION UNBER: US/09/184,216
NUMBER OF SEQ ID NOS: 8
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; NAME/KEY: Unknown
; LOCATION: 2689
; OTHER INFORMATION: Any nucleotide
US-09-184-216-1
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TYPE: DNA
ORGANISM: Human
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US-09-184-216-1
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881 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG
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                                                              484 ATGCTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAT
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Pred. No. 0;
1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09723749
; SEQUENCE 1, Application US/09723749
; GREERAL INFORMATION:
APPLICANT: Ferrara, Napoleone
; APPLICANT: Ferrara, Napoleone
; TITLE OF INVENTION: POLYPEPTIDES HOWOLOGOUS TO VEGF AND BMPI
; TILE OF INVENTION: POLYPEPTIDES HOWOLOGOUS TO VEGF AND BMPI
; CURRENT FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: US 09/265,686
; PRIOR PILING DATE: 1998-03-10
; PRIOR PILING DATE: 1998-03-17
; PRIOR FILING DATE: 1998-03-17
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NOS: 8
                                                                                                                                                                    1504 TAAACTTGTGTCATGCTGATAGGACAGACTGGA 1536
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), OTHER INFORMATION: Any nucleotide
US-09-723-749-1
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Best Local Similarity 99.9%;
Matches 1532; Conservative
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881 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG 940
                                                  604 TTTTTGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTAT
                                                                                                                                                                                                 1001 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACACGGATA
                                                                                                                                                                                                                                                                                                                                                                                          TCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAATACCACGAGG
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                                                                                                                                                             664 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA
                                                                                                                                                                                                                                                                            724 CCATTITCTGGCCAGGTIGTCTCCTGGTTAAACGCTGTGGGGAACTGTGCCTGTTGTC
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GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAATTATTACTGTGTGTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATATTC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401 GAATTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATC 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AIGCTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGAT 543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGIAGAAGIIGAGGAACCCAGIGAIGGAACIAIAIIAGGGCGCCIGGIGIGGIICIGGIA 303
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                                                                                                           GEGUENCE 1, Application US/10178442

GENERAL INFORMATION:

APPLICANT: Rerrara, Napoleone

APPLICANT: REPRESSION:

TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMPI
FILE REFERENCE: 1169-112USD2

CURRENT APPLICATION NUMBER: US/10/178,442

CURRENT FILING DATE: 1999-024

PRIOR APPLICATION NUMBER: US 09/265,686

PRIOR PILING DATE: 1999-03-10

PRIOR PILING DATE: 1998-11-02

PRIOR PLING DATE: 1998-11-02

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  1841 TAAACTTGTGTCATGCTGATAGGACAGACTGGA 1873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 2825
                                                                                   RESULT 10
US-10-178-442-1
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1087 CCATTITICTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACTGTGCCTGTTGTC 1146
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TIGTAGAAGTIGAGGAACCCAGTGAIGAACTATATTAGGGGGGCTGGTGGTTCTGGTA 666
                                                                                                                                                                                                                    424 CAGAAGCIGIGAGICCITCAGIGCIACCCCCTICAGCITIGCCACTGGACCIGCITAAIA 483
                                                                                                                                                                                                                                                                                                                                                                                                                                         604 ITTTTGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTAT 663
                                                                                  CTGTACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATG 363
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                                                                                                                    CTGTACCCAGGAAAACCAGTTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATG
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APPLICANT: Goddowski, Paul J.
APPLICANT: Goddowski, Paul J.
APPLICANT: Goddowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
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APPLICANT: Watanabe, Colin K
APPLICANT: SHORY ENGREE BOOK STORE BNCODING THE SAME
FILE REFERENCE: P33.08.1C3.1
CURRENT APPLICATION NUMBER: PCT/US01/43523
CURRENT APPLICATION NUMBER: 60/049911
FRIOR FILING DATE: 1997-06-16
FRIOR APPLICANTION NUMBER: 60/05914
FRIOR FILING DATE: 1997-09-17
FRIOR PRILING DATE: 1997-09-17
FRIOR PRILING DATE: 1997-09-17
FRIOR FILING DATE: 1997-09-17
FRIOR APPLICATION NUMBER: 60/05915
FRIOR FILING DATE: 1997-09-17
FRIOR APPLICATION NUMBER: 60/05916
FRIOR FILING DATE: 1997-09-17
FRIOR FILING DATE: 1997-09-17
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FRIOR FILING DATE: 1997-09-19
FRIOR APPLICATION NUMBER: 60/059588
FRIOR FILING DATE: 1997-09-19
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FRIOR APPLICATION NUMBER: 60/059588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: 2715
; OTHER INFORMATION: unknown base
PCT-US01-43523-285
                                                                                       Gao, Wei-Qiang
Gerritsen, Mary E.
        DeForge, Laura
Desnoyers, Luc
Filvaroff, Ellen
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Score 1532.6;
99.84;
Query Match
Best Local Similarity 99.9°
Matches 1532; Conservative
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                                                                                                                                  1687 CHGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAAACTCTAAAGCTCCATGTCCTGGG 1746
                                      CCTAAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTGCTCATATTCACATATGTAA 1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P333 OUTOER: P375 OUTOER
CURRENT APPLICATION NUMBER: PCT/US02/24563
CURRENT FILING DATE: 2002-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILLING DATE: 2002-08-02

PRIOR APPLICATION NUMBER: 60/049911

PRIOR FILING DATE: 1997-06-18

PRIOR FILING DATE: 1997-06-18

PRIOR FILING DATE: 1997-08-26

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059115

PRIOR PILING DATE: 1997-09-17

PRIOR PILING DATE: 1997-09-17

PRIOR PILING DATE: 1997-09-17

PRIOR PILING DATE: 1997-09-17

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                                                                                                                                                                                                                     1867 TAAACTTGTGTCATGCTGATAGGACAGACTGGA 1899
                                                                                                                                                                                                                                                                                                           Sequence 285, Application PC/TUS0224563 GENERAL INFORMATION:
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COTHER INFORMATION: unknown base
PCT-US02-24563-285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maureen
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gerritsen, Mary E.
Goddard, Audrey
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Wood, William
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Gurney, Austin L.
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Filvaroff, Ellen
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Smith, Victoria
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ORGANISM: Homo Sapien
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DB 1; Length 2849;
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LOCATION: 2715
OTHER INFORMATION: unknown base
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Best Local Similarity 99.9%
Matches 1532, Conservative
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                                                                                                                                                                                                                                             NAME/KEY: unsure
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                                                                                                            1204 ATGTTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGG 1263
                                                                                                                                                                                                ATGITGIATIAAATAGATCACCAGCTAGITTCAGAGITACCATGIACGIATTCCACTAGC 1626
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APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3330R1C331
CURRENT APPLICATION NUMBER: PCT/US01/43523
CURRENT APPLICATION NUMBER: PCT/US01/43523
CURRENT FILING DATE: 2002-10-02
PRIOR PELICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-08-26
PRIOR FILING DATE: 1997-09-26
PRIOR FILING DATE: 1997-09-17
PRIOR PELICATION NUMBER: 60/059115
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PRIOR PELICATION NUMBER: 60/059122
                                               GATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCT
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Stewart, Timothy A.
Tumas, Daniel
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Goddard, Audrey
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Gurney, Austin L.
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Wood, William
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Filvaroff, Ellen
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1027 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGAAGAACTAAAGAAAAAAACCGATA 1086
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PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
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PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059352
PRIOR APPLICATION NUMBER: 60/059368
PRIOR PILING DATE: 1997-09-19
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Pred. No. 0;
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967 TITITGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTAT 1026
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TITLE OF INVENTION: Treating Ocular Diseases; FILE REFERENCE: P2632; CURRENT APPLICATION NUMBER: US/09/267,213; CURRENT FILING DATE: 1999-03-12; NUMBER OF SEQ ID NOS: 41; SEQ ID NO 1; SEQ ID NO 1; LEMETH: 2849; TYPE: DNA; ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                      Query Match
99.8%; Score 1532.6;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1532; Conservative 1; Mismatches
                                                                                                                                                                                        FEATURE:
NAME/KEY: unknown
LOCATION: 2715
OTHER INFORMATION: unknown base
US-09-267-213-1
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                                                                                                                                                                                                                                                 December 1. Application US/09267213
GENERAL INFORMATION:
APPLICANT: Ferrara, Napoleone
APPLICANT: Goddard, Audrey
APPLICANT: Hebert, Caroline
APPLICANT: Hebert, Milliam
APPLICANT: Hebert, Rhona
APPLICANT: Klein, Robert D.
APPLICANT: Klavin, Ivar J.
APPLICANT: Klavin, Ivar J.
APPLICANT: Klavin, Ivar J.
APPLICANT: Wood, Sophia S.
APPLICANT: Laffeur, Monique
APPLICANT: Laffeur, Monique
APPLICANT: Laffeur, Monique
APPLICANT: Mood, William I.
TITLE OF INVENTION: Method of Preventing the Death of Retinal Neurons and
                                                                                                                                                                                                                                                                                                                                                                                                                                              CGTATECGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTTCAG
  CCATTITICIGGCCAGGITGTCTCCTGGTTAAACGCTGTGGTGGGAACTGTGCCTGTTGTC
                            CCATTITICINGCCAGGITGICICCTGGTTAAACGCTGTGGGGGAACTGTGCCTGTTGTC
                                                                               TCCACAATTGCAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAATACCACGAGG
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; PRIOR FILING DATE: 1998-03-11 ; PRIOR APPLICATION NUMBER: US 60/077,791 ; PRIOR FILING DATE: 1998-03-12 ; PRIOR APPLICATION NUMBER: US 60/078,004 ; PRIOR FILING DATE: 1998-03-13 ; PRIOR PRICATION NUMBER: US 09/040,220 ; PRIOR FILING DATE: 1998-03-17 ; PRIOR PELICATION NUMBER: US 60/078,886 ; PRIOR FILING DATE: 1998-03-20	APPLICATION NUMBER PILING DATE: PPLICATION NUMBER FILING DATE: APPLICATION NUMBER FILING DATE: APPLICATION NUMBER	998-03-25 US 60/079,6 998-03-26 US 60/079,7 US 60/079,7 US 60/079,6 US 60/079,6		FILING DATE: 1998-03-31 FILING DATE: US 60/080, FILING DATE: US 60/080, APPLICATION NUMBER: US 60/080, FILING DATE: 1998-03-31 APPLICATION NUMBER: US 60/080, APPLICATION NUMBER: US 60/080, FILING DATE: 1998-03-31	APPLICATION NUMBER APPLICATION DATE: APPLICATION NUMBER FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: APPLICATION NUMBER APPLICATION NUMBER	APPLICATION NUMBER: 1998-04-08
Db	964 ATCACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCA	Db   1387 CGTATGCGTTATCTCCATCCTTAATCTCAGGTGCTTCAAGGACCTTTCATCTTCAG 1446	1204 ATCTTGTATTAAATAGATCACCA 	Oy         1324 CTGTGCAAGTGACCCCGATTCCGTTGCTTAACTCTAAAGCTCCATGTCTGGG 1383           Db         1687 CTGTGCAAGTGACCTGATTCGTTGCTTGCTTCAAGTCTCCAAGTTCTGGG 1746           Oy         1384 CCTAAAATCGTATAAATCTGGATTTTTTTTTTTTCCTCATATGTAA 1443           Db         1747 CCTAAAATCGTATAAATCTGGATTTTTTTTTTTTTTTTT	QY         1444 ACCAGAACAITCTATGTACTACAAACTGGTTTTTAAAAAGGAACTATGTTGCTATGAAT 1503           DD         1807 ACCAGAACAITCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAAT 1866           QY         1504 TAAACTTGTGTCATGCTGATAGGACAGACTGGA 1536           DD         1867 TAAACTTGTGTCATGCTGATAGGACAGACTGGA 1899	RESULT 15  US-09-380-138-487  US-09-380-138-487  US-09-380-138-487  GENERAL INFORMATION:  APPLICANT:  APPLICANT:  APPLICANT:  APPLICANT:  APPLICANT:  APPLICANT:  APPLICANT:  APPLICANT:  APPLICANT:  APPLICANT:  APPLICANT:  APPLICANT:  APPLICANT:  APPLICANT:  Baker, Kevin P.  TITLE OF INVENTION:  NOWEH POLYOPETION OF POLY

Page 17

NUMBER: US 60/082,700 NUMBER: US 60/082,804 1998-04-22 NUMBER: US 60/082,704 1998-04-23 NUMBER: US 60/082,767 1998-04-23 NUMBER: US 60/082,796 NUMBER: US 60/083,336 NUMBER: US 60/083,336 NUMBER: US 60/083,332 NUMBER: US 60/083,322	NUMBER:  UMBER:  1998-04-  UMBER:  1998-04-  UMBER:  1998-04-  UMBER:  1998-04-  UMBER:  UMBER	
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427 GAATTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATATTATC 486
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Best Local Similarity 99.9%; Score 1532.6; DB 20; Length 2849;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1532; Conservative 1; Mismatches 0; Indels 0;
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: US 60/085,700
PRIOR PILING DATE: 1998-05-18
PRIOR PILING DATE: US 60/086,023
PRIOR FILING DATE: 1998-05-18
PRIOR FILING DATE: 1998-05-22
PRIOR PILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: US 60/086,414
PRIOR APPLICATION NUMBER: US 60/086,302
PRIOR FILING DATE: 1998-05-22
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PRIOR PILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: US 60/087,208
PRIOR PILING DATE: 1998-05-28
PRIOR PILING DATE: 1998-05-28
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PRIOR FILING DATE: 1998-05-38
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PRIOR FILING DATE: 1998-09-11
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GGCAGTTGGACT 	TTTTGGAAGA/             TTTTTGGAAGA/	ACAGCTGCACA(                 ACAGCTGCACA(	CCATTITCIGG            CCATTITCIGG	TCCACAATTGCI            TCCACAATTGCI	TCCTTCAGTTG	CCCTGGAGCAC	ATCACCACCAGG	CGTATGCGTTA'	GATTTACAGTG            GATTTACAGTG	CTTTTGAGAGG	ATGTTGTATTA            ATGTTGTATTA	TGGGTTCTGTA'             TGGGTTCTGTA'	CTGTGCAAGTG             CTGTGCAAGTG	CCTAAAATCGT.                CCTAAAATCGT.	ACCAGAACATTO		
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Search completed: November 26, 2003, 08:54:58 Job time : 3284.48 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

November 26, 2003, 00:11:41; Search time 284.211 Seconds (without alignments) 9894.257 Million cell updates/sec Run on:

US-09-852-209A-4 1536 Title: Perfect score:

1 cgggtaaattccagttttcc.....tgctgataggacagactgga 1536 Sequence:

Gapop 10.0 , Gapext 1.0 IDENTITY NUC Scoring table:

Total number of hits satisfying chosen parameters: 2523179 seqs, 915383134 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pending\_Patents\_NA\_New:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		ð			SOUTHWINES	
Result No.	Score		Length	DB	QI	Description
т.	1531	99.7	3007	! -	PCT-US03-26491-58	: .
7	1531	99.7	m	9	US-10-648-593-58	58.
m	1531	99.7		7	US-60-487-610-231	231
4	1531	99.7	c	7	485-450	
Ω	1531		m	7	0-507-511	208
9	1529.4		N	Ŋ	US-09-830-320A-8	8, App
7	1511		1	Ŋ	US-09-457-066-1	H
æ	1511		٦	'n	928-60	32
6	1511			9	US-10-664-432-1	Sequence 1, Appli
10	955.6		Н	വ	ŝ	50
11	721			Ŋ	US-09-457-066-42	42
12	721		3571	'n	US-09-876-813-34	34
13	721	46.9		9	US-10-664-432-3	'n
14	694.4	45.2	223	7	US-60-487-610-19346	19
15	694.4	45.2	221	7	US-60-485-450-11913	Sequence 11913, A
16	684.4	44.6	-	Ŋ	US-09-457-066-6	6, Appl
17	621	40.4	918	Н	PCT-US00-28803-6	ø
18	200.6	13.1		7	US-60-487-610-5054	5054
19	200.6	13.1		7	US-60-487-610-5055	Sequence 5055, Ap
20	200.6	13.1		~	US-60-487-610-32070	32070.
21	200.6	13.1		۲	US-60-487-610-32126	32126,
22	200.6	13.1		7	-60-485-4	3280,
23	200.6	13.1		7	US-60-485-450-3281	Sequence 3281, Ap
24	200.6	•	201	~	US-60-485-450-19014	19014,
25	200.6	13.1	201	2	US-60-485-450-19070	19070.
26	2007	13.0	201	7	US-60-487-610-5053	Sequence 5053, Ap

		~	nce 6, Appli	Ο,	ace 5052, Ap	ice 32073, A		ice 19017, A	nce 7, Appli	25,	ıce 3, Appli	nce 3, Appli	ice 36, Appl	nce 1, Appli	H	nce 5, Appli	9	ce 11, Appl
Sequence	Sequence	Sequence	Seguence	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence
US-60-487-610-32074	US-60-485-450-3279	US-60-485-450-19018	US-09-876-813-6	US-09-540-233D-96491	US-60-487-610-5052	US-60-487-610-32073	US-60-485-450-3278	US-60-485-450-19017	US-10-321-962-7	US-09-876-813-52	US-10-606-055-3	US-10-321-962-3	US-09-457-066-36	US-09-876-813-1	US-10-606-055-1	US-10-321-962-5	US-10-321-962-9	US-10-321-962-11
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201	201	201	1110	135	201	201	201	201	1113	1472	1472	1829	1882	1882	1882	1587	868	462
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200.2	200.2	200.2	177.4	128	120.6	120.6	120.6	120.6	117.4	117.4	117.4	105.2	103.6	103.6	103.6	101.4	85.6	84
27	28	53	30	31	32	33	34	35	36	37	38	39	40	4.	42	43	44	45

## ALIGNMENTS

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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS TH
TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
FILE REFERENCE: D0273 PCT
CURRENT APPLICATION NUMBER: PCT/US03/26491
CURRENT APPLICATION NUMBER: PCT/US03/26491
RIOR APPLICATION NUMBER: 60/406,385
PRIOR FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 557
SQOTRAME: Patentin version 3.2
SEQ ID NO 58
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                     ; Sequence 58, Application PC/TUS0326491; GENERAL INFORMATION:
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Best Local Similarity 99.9*
Matches 1531; Conservative
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Sequence 58, Application US/10648593
| Sequence 58, Application US/10648593
| GENERAL INFORMATION:
| APPLICANT: BILISTOL NAMES SQUIBD Company |
| TITLE OF INVENTION: INFERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR |
| TITLE OF INVENTION: INFERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR |
| TITLE OF INVENTION: INFERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR |
| TITLE OF INVENTION: INFERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR |
| FILE REFERENCE: D0273 NP |
| CURRENT APPLICATION NUMBER: US/10/648,593 |
| CURRENT FILING DATE: 2002-08-26 |
| PRIOR PILING DATE: 2002-08-27 |
| NUMBER OF SEQ ID NOS: 557 |
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99.9%; Pred. No. 0;
Live 1; Mismatches 1; Indels 0
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us-09-852-209a-4.rnpn

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TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLOO1469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTMARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 231
LENGTH: 3007
                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
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; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: HUANG, Hongin:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
                                                                             TCCTTCAGTTGAGACCAAASACCGGTGTCAGGGGATTGCACAAATCACTCACCGACGTGG
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Query Match 99.7%; Score 1531; DB 7; Length 3007; Best Local Similarity 99.7%; Pred. No. 0; Matches 1528; Conservative 5; Mismatches 0; Indels 0
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TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: AM 10.081
CURRENT APPLICATION NUMBER: US/60/507,511
CURRENT PILING DATE: 2003-10-02
NUMBER OF SEQ ID NOS: 203623
SEQ ID NO 2084
LENGTH: 3007
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; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
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                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: YUE, Henry
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: CORLEY, Neil C.
APPLICANT: GUBGLER, Karl J.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: AL-YOUNG, Janice K.
APPLICANT: AL-YOUNG, Janice K.
TITLE OF INVENTION: GROWTH PACTOR RELATED MOLECULES
FILE REFERENCE: PF-0627 USN
                                                                                                                                                                                1504 TAAACTTGTGTCATGCTGATAGGACAGACTGGA 1536
                                                                                                                                                                                                                 2074 raaacricricricricricaracacacacrica 2106
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CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: US/09/830,320A
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1998-10-28
PRIOR PILING DATE: 1998-10-28
PRIOR FILING DATE: 1998-10-38
PRIOR FILING DATE: 1998-12-11
PRIOR FILING DATE: 1998-12-11
PRIOR FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PERL PROGRAM
SOFTWARE: PERL PROGRAM
SOFTWARE: PERL PROGRAM
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US-09-830-320A-8
                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09830320A
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: INCYTE GENOMICS, INC. APPLICANT: TANG, Y. TOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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956 CCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACTGTGCCTGTTGTC 1015
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                 484 AIGCIATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGAT 543
                                604 TTTTTGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTAT 663
                                                                                                                                                                                                                                                                   896 ACAGCIGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA 955
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                                                                                                            776 GGCAGTTGGACTTAGAAGATCTATATAGAGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG
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                                                                                          544 GGCAGTIGGACTIAGAAGAICIAIATAGGCCAACTIGGCAACTICTIGGCAAGGC
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                                                                             CCTABABATGGTBIBABAATCTGGBATTTTTTTTTTTTTTTTTTTGCTCATATTCACATATGTBA 1779
                                                          ACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAAT 1503
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1522; Conservative 1; Mismatches 1; Indels 1; Gaps
                                                                                                                                                                                                           US-09-457-066-1

US-09-457-066-1

Sequence 1, Application US/09457066

GENERAL INFORMATION:

APPLICANT: Gao, Zeren

APPLICANT: Hart, Charles B.:

APPLICANT: Sheppard, Paul O.

APPLICANT: Sheppard, Paul O.

APPLICANT: Sheppard, Paul O.

APPLICANT: Shepmare, Kimberly B.

APPLICANT: Gilbertson, Debra G.

APPLICANT: West, James W.

ITLE OF INVENTION: GROWTH FACTOR HOWOLOG ZVEGP3

FILE REFERENCE: 98-60

CURRENT APPLICATION NUMBER: US/09/457,066

CURRENT FILING DATE: 1999-12-07

SOFTWARE FELING DATE: P80-60

SOFTWARE: FactSEQ for Windows Version 3.0
                                                                                                                                 1504 TAAACTIGIGICAIGCIGAIAGGACAGACIGGA 1536
                                                                                                                                                    ; LOCATION: (154)...(1191)
US-09-457-066-1
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Sequence 1, Application US/10664432; GENERAL INPORMATION:
APPLICANT: Hart Charles E.
APPLICANT: Gilbertson, Debra G.
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                                                       GENERAL INFORMATION:
APPLICANT: Gilbert, Teresa
APPLICANT: Gilbert, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOWOLOG ZVEGF4
FILE REPERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/876,813
CURRENT APPLICATION NUMBER: US/09/564,595
PRIOR FILING DATE: 2001-05-03
PRIOR FILING DATE: 1999-05-03
PRIOR PILING DATE: 1999-05-03
PRIOR PLING DATE: 1999-05-03
PRIOR PLING DATE: 1999-05-03
PRIOR PLING DATE: 1999-05-03
PRIOR FILING DATE: 1999-05-04
PRIOR FILING DATE: 1999-05-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 1760
LENGTH: 1760
LENGTH: 1760
LENGTH: 1760
                                Sequence 32, Application US/09876813 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: (154)...(1191)
US-09-876-813-32
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RESULT 8
US-09-876-813-32
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                                                              604 TITITGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTAT 663
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FastSEQ for Windows Version 3.0
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SEQ ID NO 50
LENGTH: 1095
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US-09-457-066-50
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                                                                                                                                                                                                                                                                       Query Match 98.4%; Score 1511; DB 6; Length 1760; Best Local Similarity 99.8%; Pred. No. 0; Matches 1522; Conservative 1; Mismatches 1; Indels 1;
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE, TITLE OF INVENTION: LIGAMENT AND CARTILAGE FILE REFERENCE: 00-12 CURRENT APPLICATION NUMBER: US/10/664,432 CURRENT FILING DATE: 2003-09-19 NUMBER OF SEQ ID NOS: 5 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 1
LENGTH: 1760
                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (154)...(1191)
US-10-664-432-1
                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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1024 CGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAG 1083
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GENERAL INFORMATION:
APPLICANT: Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zerra Gao, Zer
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364 AATATTTTCCTTCTGAACCAGGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCA 423
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                                                                                                                                                                                                                                                                                                                                                                           Score 721; DB 5; 1
Pred. No. 4.1e-218;
                                                                                                                                                            ZVEGF3
        US-09-157-066-42

Sequence 42, Application US/09457066

GENERAL INFORMATION:
APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Sheghard, Paul O.
APPLICANT: Sheghard, Paul O.
APPLICANT: Sheghard, Paul O.
APPLICANT: Sheghard, Paul O.
APPLICANT: Sheghard, James W.
APPLICANT: Sheghard, James W.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWH PACTOR HOMOLOG ZVI
FILE REFERENCE: 98-60
CURRENT APPLICATION NUMBER: US/09/457,066
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 42
LIENGTH: 3571
                                                                                                                                                                                                                                                                                                                                                                          46.9%;
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 83.6'
Matches 817, Conservative
                                                                                                                                                                                                                                                                                                                               ; LOCATION: (1049)...(2086)
US-09-457-066-42
                                                                                                                                                                                                                                                                                      ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
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                                                                                   Gaps
                                                                                0;
                                                        Length 1095
                                                                                 Indels
                                                     tch 62.2%; Score 955.6; DB 5; sal Similarity 99.9%; Pred. No. 5.2e-293; 955; Conservative 1; Mismatches 0;
 ; FEATURE:
; OTHER INFORMATION: Fused
US-09-457-066-50
                                                    Query Match
Best Local S
Matches 955
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Length 3571; Indels 1310

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1731 TGTATGGGAAAAAAGCAAAGTGGTGAATCTGAATCTCCTCAAGGAAGAGGTAAAACTCT 1790

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US-10-664-432-3

US-10-664-432-3

Sequence 3, Application US/10664432

GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: METHODS FOR PROMOTING GROWT
TITLE OF INVENTION: LIGAMENT AND CARTILAGE
FILE REPERBURE: 00-12
CURRENT APPLICATION NUMBER: US/10/664,432
CURRENT FILING DATE: 2003-09-19
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENDER HAND 3571
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                                              1911 TCCATAATTGCCAATGAATGTCACGTGTGTCCCACGTAAGTTACAAAAAGTACCATGAGG 1970
                                                                                                                                                                                                                                                                        2031 CTCTGGAACACCACGAGGAATGTGACTGTGTGTAGAGGAAACGCAGGAGGGTAACTGC 2090
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                                                                                                   724 CCATTITCIGGCCAGGIIGICICCIGGIIAAACGCIGIGGIGGGAACIGIGCCIGIIGIC
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46.9%; Score 721; DB 5; Length 3571;
Best Local Similarity 83.6%; Pred. No. 4.1e-218;
Matches 817; Conservative 0; Mismatches 160; Indels (
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APPLICANT: Hart, Charles E.
APPLICANT: Hart, Charles E.
APPLICANT: Hart, Charles E.
APPLICANT: Bart, Charles E.
APPLICANT: SGREPBACH PAUD.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595
PRIOR PLILNG DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/564,595
PRIOR PLILNG DATE: 1999-05-03
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.0
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18-09-576-813-34
Sequence 34, Application US/09876813
GENERAL INFORMATION:
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; LOCATION: (1049)...(2086)
US-09-876-813-34
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                                                           1371 Trigragaagrigaaggagcccagrgarggaagrgrirfagaacgcrggrgrgrgrgragga 1430
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244 TIGIRGRAGITGAGGAACCCAGIGATGGAACIAIAITAGGGCGCTGGTGTGGTTCTGGTA 303
                                                                                                                             CTGTACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATG 363
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Query Match 45.2%; Score 694.4; DB 7; Best Local Similarity 97.8%; Pred. No. 1.1e-208; Matches 698; Conservative 5; Mismatches 11;
                     2107
                                                                                                                                                                                                                                                                                     ; LOCATION: (1)....(221510)
; OTHER INFORMATION: n = A,T,C
US-60-487-610-19346
964 ATCACCACCAGCAGCTC
                     2091 AGCCTTCGTAGCAGCAC
                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                 SEQ ID NO 19346
LENGTH: 221510
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                                                                                                                                             GAATTATTACTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATC
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                                                                                                4 GTAAATICCAGITITCCAGCAACAAGAACAGAACGAGIACAAGAICCTCAGCAIGAGA
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                                                    Length 3571;
                                                  Score 721; DB 6; Length 35
Pred. No. 4.1e-218;
0; Mismatches 160; Indels
                                                   Query Match
Best Local Similarity 83.6%;
Matches 817; Conservative
       ) NAME/KEY: CDS
; LOCATION: (1049)...(2086)
US-10-664-432-3
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Sequence 19346, Application US/60487610
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: GENETIC, Michele
APPLICANT: GENETIC, MICHELE
APPLICANT: HUANG, HONGIN
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FASTSEQ for Windows Version 4.0
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NAME/KEY: misc_feature

| LOCATION: (1)...(221510)

| OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-

US-60-485-450-11913
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                                                                                                                                                                                                                                                                                                  APPLICANT: CREGILL, Michele
APPLICANT: CHANG, Sheng-Yung
TITLE OF INVENTION: GENERALIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
TITLE OF INVENTION: VIRUS-INPECTED SUBJECTS, METHODS OF DETECTION AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CL001470
CURRENT APPLICATION NUMBER: US/60/485,450
CURRENT FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 47859
SOFTWARE: FRAFESQ for Windows Version 4.0
SEQ ID NO 11913
1423 TGCTCATATTCACATATGTAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAA 1482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                823 ITACTAAAAATACCACGAGGTCCTTCAGTTGAGACCAAASACCGGTGTCAGGGGATTGC 882
                                                                                      1483 AGGAACTAIGITGCTAIGAATTAAACTIGIGTCATGCTGATAGGACAGACTGGA 1536
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                                                                                                                                                                                                                                                      ; Sequence 11913, Application US/60485450; GENERAL INFORMATION:
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US-60-485-450-11913
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Search completed: November 26, 2003, 09:11:07 Job time : 288.211 secs

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Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Decortes 2826 bp mRNA linear HTC 13-JAN-2003 Home sapiens, Similar to platelet-derived growth factor, C Decorting Control of Second Control Decort Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Co
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1 (bases 1 to 2826)
Straubberg.R.
Direct Submission
Submitted (23-DEC-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                 BG681390 6
BI870535 6
AK052947 b
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BQ694737
BG430400
BM827309
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BE958470
BU459467
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BF670092
BU259419
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